

# SCORE Search Results Details for Application 10591347 and Search Result 20110118\_143603\_seq2sub1624a.rng.

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GenCore version 6.3  
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2011, 21:51:00 ; Search time 1435 Seconds  
(without alignments)  
50622.995 Million cell updates/sec

Title: SEQ2SUB1624A  
Perfect score: 3424  
Sequence: 1 aggatcagaacaatgcctcc.....taaactagttcattcaaaa 3424

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18225500 seqs, 10608060480 residues

Total number of hits satisfying chosen parameters: 36451000

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_201023:  
1: geneseqn1:  
2: geneseqn2:  
3: geneseqn3:  
4: geneseqn4:  
5: geneseqn5:  
6: geneseqn6:  
7: geneseqn7:  
8: geneseqn8:

9: geneseqn9:\*

## SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	3422.4	99.9	3424	1	AAS14365	Aas14365 cDNA enco
2	3422.4	99.9	3424	1	ABL59523	Ab159523 Human pho
3	3422.4	99.9	3424	2	ADE85076	Ade85076 Farnesyl
4	3422.4	99.9	3424	4	ADZ00490	Adz00490 p110-beta
5	3422.4	99.9	3424	4	AEH10445	Aeh10445 PIK3CA cD
6	3422.4	99.9	3424	4	AED31618	Aed31618 cDNA (SEQ
7	3422.4	99.9	3424	4	AEG93388	Aeg93388 Human tum
8	3410.4	99.6	3412	1	AAQ51156	Aaq51156 Human p11
9	3410.4	99.6	3412	4	AED31617	Aed31617 cDNA (SEQ
10	3410.4	99.6	3423	3	ADU05935	Adu05935 Novel bro
11	3338	97.5	3426	6	ARC02473	Arc02473 DNA fragm
12	3338	97.5	3724	4	AEK54940	Aek54940 Human PIK
13	3338	97.5	3724	5	AER29796	Aer29796 Breast ca
14	3338	97.5	3724	7	ARV60468	Arv60468 Human PIK
15	3338	97.5	3724	7	ARW65283	Arw65283 Human PIK
16	3338	97.5	3724	7	ATM52123	Atm52123 Human PIK
17	3338	97.5	3724	7	ATS16021	Ats16021 Human pho
18	3338	97.5	3724	8	AWY98731	Awy98731 Human PIK
19	3338	97.5	3724	8	AWY98891	Awy98891 Human PIK
20	3338	97.5	3724	8	AWY98894	Awy98894 Human PIK
21	3338	97.5	3724	9	AXU25358	Axu25358 Human pho
22	3338	97.5	3724	9	AYE41305	Aye41305 Human PIK
23	3279.4	95.8	4326	8	AWY98838	Awy98838 Human PIK
24	3205.4	93.6	3207	2	ADH68168	Adh68168 DNA encod
25	3205.4	93.6	3207	4	AEF64785	Aef64785 Human pho
26	3145	91.9	7923	8	AWO77361	Awo77361 Expressio
27	3144.6	91.8	3207	7	ARL60529	Arl60529 Human pho
28	3143	91.8	3207	4	AEK13519	Aek13519 Phosphati
29	3141.4	91.7	3207	4	AEK13514	Aek13514 Phosphati
30	3141.4	91.7	3207	4	AEK13515	Aek13515 Phosphati
31	3137	91.6	3498	1	AAQ57012	Aaq57012 PtdIns 3-
32	3118.8	91.1	3210	4	AEK13511	Aek13511 Phosphati
33	3007	87.8	3207	1	AAQ51155	Aaq51155 p110 cDNA
34	2640.6	77.1	3207	8	AWY98836	Awy98836 Human PIK
35	2640.6	77.1	3207	8	AWY98892	Awy98892 Human PIK
36	1686	49.2	8421	2	ACN43202	Acn43202 Human dia
37	1515.8	44.3	2397	1	AFS82080	Afs82080 Human tra
38	1183.4	34.6	1792	3	ADR39810	Adr39810 Human kin
39	699	20.4	2872	8	AWY98893	Awy98893 Human PIK
40	564	16.5	741	1	AAA02190	Aaa02190 Human col
41	564	16.5	741	4	AGD33161	Agd33161 Human pol
42	530	15.5	716	4	AEK18520	Aek18520 Human PIK
43	459.2	13.4	3213	1	AAC65690	Aac65690 Human PI3

44	459.2	13.4	3213	1	AAS14366
45	459.2	13.4	3213	1	ABV78026

Aas14366	cDNA	enco
Abv78026	Hypoxia-r	

## ALIGNMENTS

RESULT 1

AAS14365

ID AAS14365 standard; cDNA; 3424 BP.

XX

AC AAS14365;

XX

DT 11-JUN-2007 (revised)

DT 12-MAR-2002 (first entry)

XX

DE cDNA encoding human p110alpha isoform of PI3-kinase.

XX

KW Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform; LASP-1;

KW cancer; inflammatory disease; ophthalmic disorder; SH3 domain;

KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;

KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..3219

FT /\*tag= a

FT /product= "p110alpha isoform of PI3-kinase"

XX

PN WO200185986-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-US015065.

XX

PR 10-MAY-2000; 2000US-0203346P.

XX

PA (ICOS-) ICOS CORP.

XX

PI Sadhu C;

XX

DR WPI; 2002-075252/10.

DR P-PSDB; AAU09687.

DR PC:NCBI; gi472990.

DR PC\_ENCPRO:NCBI; gi472991.

XX

PT Identifying a modulator of p110delta polypeptide binding to SH3 domain-containing polypeptides e.g. LASP-1, comprising allowing the binding

PT partners to interact in the presence and absence of a test compound.

XX  
PS Example 1; Page 55-60; 85pp; English.

CC The present invention relates to identifying a modulator of the phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to the catalytic subunit via a SH3 domain-containing polypeptide such as LASP-1. CC Also described are methods of assaying the specific binding affinity of the PI3-kinase binding partner. Such modulators are useful for the treatment of diseases characterised by the undesirable or excessive activity of PI3Kdelta. For example the modulators can be used for inhibiting the growth or proliferation of cancer cells (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues, Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid arthritis), ophthalmic disorders (e.g. allergic conjunctivitis), autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory dermatoses (e.g. contact dermatitis; central or peripheral nervous system inflammatory disorders (e.g. meningitis), bacterial pneumonia, and Type I diabetes mellitus. The present sequence encodes for human p110alpha isoform of PI3k

CC  
Revised record issued on 11-JUN-2007 : Enhanced with precomputed information from BOND.

XX  
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 1; Length 3424;  
Best Local Similarity 99.9%;  
Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGCATCCACTTGATG 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGCATCCACTTGATG 60

Qy 61 CCCCAAGAACATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGTACTTAGAATGC 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 CCCCAAGAACATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGTACTTAGAATGC 120

Qy 121 CTCCGTGAGGCTACATTAGTAACATAAGCATGAACATTAAAGCAAGAAATAC 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 CTCCGTGAGGCTACATTAGTAACATAAGCATGAACATTAAAGCAAGAAATAC 180

Qy 181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCGTAAGTGTACCCAAGAA 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCGTAAGTGTACCCAAGAA 240

Qy 241 GCAGAAAGGGAGAATTTTGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA 300  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db	241	GCAGAAAGGGAGAATTTTGATGAAACAAGACGACTTGTGATCTCGGCTTTCAA	300
Qy	301	CCATTTTAAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301		
Db	301	CCATTTTAAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361		
Db	361	ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTCCGAAGAAATATTCTTAATGTTGTAAGAGCTGTGGATCTTAGGGATCTT	480
Db	421		
Db	421	CAGGACTCCGAAGAAATATTCTTAATGTTGTAAGAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGCTATCCGCCACATGTAGAATCTCACAGAG	540
Db	481		
Db	481	AATTCACCTCATAGTAGAGCAATGTATGCTATCCGCCACATGTAGAATCTCACAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCAAAATAATGGTGATTGGGTA	600
Db	541		
Db	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCAAAATAATGGTGATTGGGTA	600
Qy	601	ATAGTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCAGACTGTG	660
Db	601		
Db	601	ATAGTTCTCCAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCAGACTGTG	660
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661		
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Db	721		
Db	721	GAACAATTAAACTCTGTGTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Qy	781	TGTGATGAAACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGCTGT	840
Db	781		
Db	781	TGTGATGAAACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGCTGT	840
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	841		
Db	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901		
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGTTATAATAGAGCACTCAGAATA	1020
Db	961		
Db	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGTTATAATAGAGCACTCAGAATA	1020

Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATTCGAGACATTGACAAGATTATGTT	1080
Db	1021		
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081		
Qy	1141	CCTTGTTCATCCAGGTGGAATGGAATGGCTGAATTATGATATACATTCTGTACCTT	1200
Db	1141		
Qy	1201	CCTCGTGCTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201		
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261		
Qy	1321	GTATCTGGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321		
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAAACCTCATGCTTAGAGTTGGAG	1440
Db	1381		
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441		
Qy	1501	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501		
Qy	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1561		
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTCTATGGAGTCACAGACAC	1680
Db	1621		
Qy	1681	TATTGTGTAACATCCCCGAAATTCTACCCAAATTGCTTGTCTGTTAAATGGAATTCT	1740
Db	1681		

Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTAATTCACTGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTAATTCACTGCTAGTA	1920
Qy	1921	CAGGTCTAAAATATGAACAATATTGGATAACTGCTTGTGAGATTTACTGAAGAAA	1980
Db	1921	CAGGTCTAAAATATGAACAATATTGGATAACTGCTTGTGAGATTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGACTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGACTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGTCGTGCATGTGGG	2100
Qy	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTAACACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTAGTT	2220
Db	2161	GACATTCTAACACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTAGTT	2220
Qy	2221	GAGCAAATGAGGCAGCCAGATTCTATGGATGCCCTACAGGGCTTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCAGCCAGATTCTATGGATGCCCTACAGGGCTTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGAAATTATGTCTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGAAATTATGTCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Qy	2401	AATGAGATCATTTAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATTTAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATCTGGAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520

Db	2461	ATTCGTATTATGGAAAATATCTGGAAATCAAGGCTTGATCTCGAATGTTACCTTA	2520
Qy	2521	GGTTGTCTGCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCCGTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCACTGCAAAGGCCGTTGAAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTCATGTGCTGGACTGTGAGCTACCTTCATTTGGGAATTGGAGATCGT	2760
Db	2701	TTTACACGTTCATGTGCTGGACTGTGAGCTACCTTCATTTGGGAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTGAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Qy	2821	TTTTGGATCACAAGAAGAAAAAATTGGTTATAACGAGAACGTGTCGCATTGTTTG	2880
Db	2821	TTTTGGATCACAAGAAGAAAAAATTGGTTATAACGAGAACGTGTCGCATTGTTTG	2880
Qy	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGCCAAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGCCAAAGAATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACACGATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACACGATGCCAAT	3000
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Db	3001	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Qy	3061	GATGACATTGCATACATTGAAAGACCCTAGCCTAGATAAAACTGAGCAAGAGGCTTTG	3120
Db	3061	GATGACATTGCATACATTGAAAGACCCTAGCCTAGATAAAACTGAGCAAGAGGCTTTG	3120
Qy	3121	GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240

Db	3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	
Qy	3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAACT	3360
Db	3301	
Qy	3361 ATATAATTAAATAATGTAAACGCACACAGGGTTTGATAGCACTTAAACTAGTTCATTC	3420
Db	3361	
Qy	3421 AAAA 3424	
Db	3421       AAAA 3424	

## RESULT 2

ABL59523

ID ABL59523 standard; cDNA; 3424 BP.

XX

AC ABL59523;

XX

DT 11-JUN-2007 (revised)

DT 16-JUL-2002 (first entry)

XX

DE Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.

XX

KW Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme; tumour; lipid associated gene; lipid metabolism; lipid synthesis; chromosome 3q26.3; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200227028-A1.

XX

PD 04-APR-2002.

XX

PF 27-SEP-2001; 2001WO-US030366.

XX

PR 28-SEP-2000; 2000US-00676052.

XX

PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.

XX

PI Skinner MK, Patton JL, Chaudhary J;

XX

DR WPI; 2002-405056/43.

DR PC:NCBI; gi472990.

DR PC\_ENCPRO:NCBI; gi472991.

XX

PT Identifying tumor characteristics in a tissue sample taken from a patient, involves determining the copy number or expression level of genes associated with lipid metabolism, synthesis or action.

XX

PS Example 1; Page 82-83; 113pp; English.

XX

CC The present invention describes a method for identifying tumour characteristics, comprising measuring a copy number or expression level CC of at least two genes associated with lipid metabolism, synthesis, or CC action in cells from a patient tissue sample, and comparing the results CC with a copy number or expression level of the genes in a normal cell. CC Also described is an array of nucleic acid polymers immobilised on a solid support, comprising a solid support, at least two different nucleic CC acid polymers which are each specific for a different gene associated CC with lipid metabolism, synthesis or action, where each nucleic acid CC polymer is located at a predetermined position on the solid support, and CC the array comprises nucleic acid polymers which are specific for less CC than 100 genes other than the selected genes. The method is useful for CC determining tumour characteristics in a tissue sample taken from a patient. The present sequence represents a human lipid-associated gene CC related cDNA sequence, which is used in the exemplification of the CC present invention

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed CC information from BOND.

XX

SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match	99.9%	Score	3422.4	DB	1	Length	3424
Best Local Similarity	99.9%						
Matches	3423	Conservative	0	Mismatches	1	Indels	0
						Gaps	0
Qy	1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGA	ACTGTGGGCATCCACTTGATG	60			
Db	1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGA	ACTGTGGGCATCCACTTGATG	60			
Qy	61	CCCCCAAGAATCCTAGTGGATGTTACTACCAAATG	GAATGATAGTGACTTTAGAATGC	120			
Db	61	CCCCCAAGAATCCTAGTGGATGTTACTACCAAATG	GAATGATAGTGACTTTAGAATGC	120			
Qy	121	CTCCGTGAGGCTACATTAGTA	ACTATAAGCATGAACTATTAAAGAAGCAAGAAAATAC	180			
Db	121	CTCCGTGAGGCTACATTAGTA	ACTATAAGCATGAACTATTAAAGAAGCAAGAAAATAC	180			
Qy	181	CCTCTCCATCAACTTCTCAAGATGA	ATCTTCTACATTTCGTAAGTGTACCAAGAA	240			

Db	181 CCTCTCCATCAACTTCTCAAGATGAATCTCTTACATTTCTGTAAGTGTACCCAAGAA	240
Qy	241 GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTCAA	300
Db	241 GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTCAA	300
Qy	301 CCATTTAAAAGTAATTGAACCACTAGGCACCCTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301 CCATTTAAAAGTAATTGAACCACTAGGCACCCTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361 ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361 ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421 CAGGACTTCCGAAGAAATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421 CAGGACTTCCGAAGAAATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481 AATTCAACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAAGAG	540
Db	481 AATTCAACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAAGAG	540
Qy	541 CTGCCAAAGCACATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Db	541 CTGCCAAAGCACATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Qy	601 ATAGTTCTCAAATAATGACAAGCAGAAGTATACCTGCTAAACATCAACCATGACTGTGTG	660
Db	601 ATAGTTCTCAAATAATGACAAGCAGAAGTATACCTGCTAAACATCAACCATGACTGTGTG	660
Qy	661 CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAACTATGTTCTATCATCT	720
Db	661 CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAACTATGTTCTATCATCT	720
Qy	721 GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAGTGTGTGGA	780
Db	721 GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAGTGTGTGGA	780
Qy	781 TGTGATGAATACCTCTAGAAAAATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781 TGTGATGAATACCTCTAGAAAAATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841 ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	841 ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Qy	901 CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901 CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960

Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTIONGGTCAGCAGTGTGGTAAAGTCCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTIONGGTCAGCAGTGTGGTAAAGTCCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGACAGCTCAAAGCAATTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGACAGCTCAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680

Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Qy	1921	CAGGTCTAAACATATTGGATAACTTGCTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCTAAACATATTGGATAACTTGCTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTGGCATTAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTGGCATTAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTCATGTGGG	2100
Qy	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTA	2160
Db	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTA	2160
Qy	2161	GACATTCTAAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2161	GACATTCTAAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCACCAGATTCTGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCACCAGATTCTGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Qy	2401	AATGAGATCATTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460

Db	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGCAATCGGTGACTGTGTGGACTTATTGAGGTGGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGCAATCGGTGACTGTGTGGACTTATTGAGGTGGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCCTGAAAGGTGACTGCAGTTAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCACTGCAAAGGCCTGAAAGGTGACTGCAGTTAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTCATGTGCTGGACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701	TTTACACGTTCATGTGCTGGACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGCCATTGTTTG	2880
Db	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGCCATTGTTTG	2880
Qy	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGTATTGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGTATTGACAGCATGCCAAT	3000
Qy	3001	CTCTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Db	3001	CTCTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Qy	3061	GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3061	GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180

Db 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240  
|||

Db 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA 3300  
|||

Db 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA 3300

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACT 3360  
|||

Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACT 3360

Qy 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTC 3420  
|||

Db 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTC 3420

Qy 3421 AAAA 3424  
|||

Db 3421 AAAA 3424

## RESULT 3

ADE85076

ID ADE85076 standard; DNA; 3424 BP.

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AC ADE85076;

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DT 11-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Farnesyl transferase inhibitor modulated leukemia associated gene #295.

XX

KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;

KW quinolinone; leukemia; cancer.

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OS Homo sapiens.

XX

PN WO2003038129-A2.

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PD 08-MAY-2003.

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PF 30-OCT-2002; 2002WO-US034784.

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PR 30-OCT-2001; 2001US-0338997P.

PR 30-OCT-2001; 2001US-0340081P.

PR 30-OCT-2001; 2001US-0340938P.

PR 30-OCT-2001; 2001US-0341012P.

XX  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 XX  
 PI Raponi M;  
 XX  
 DR WPI; 2003-513497/48.  
 DR PC:NCBI; gi472990.  
 DR PC\_ENCPRO:NCBI; gi472991.  
 XX  
 PT Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.  
 XX  
 PS Disclosure; SEQ ID NO 295; 346pp; English.  
 XX  
 CC The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.  
 CC  
 CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed information from BOND.  
 XX  
 SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 3422.4; DB 2; Length 3424;  
 Best Local Similarity 99.9%;  
 Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGCATCCACTTGATG 60  
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGCATCCACTTGATG 60  
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 61 CCCCCAAGAATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120  
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 CCCCCAAGAATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120  
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 121 CTCCGTGAGGCTACATTAGTAACATAAAAGCATGAACATTAAAGAAGCAAGAAAATAC 180  
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CTCCGTGAGGCTACATTAGTAACATAAAAGCATGAACATTAAAGAAGCAAGAAAATAC 180  
     |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTGTAAGTGTACCAAGAA 240  
     |||||||||||||||||||||||||||||||||||||||||||||||||||

Db	181 CCTCTCCATCAACTTCTCAAGATGAATCTCTTACATTTCTGTAAGTGTACCCAAGAA	240
Qy	241 GCAGAAAGGGAGAATTTCGATGAAACAAGACGACTTGTGATCTCGGTTTCAA	300
Db	241 GCAGAAAGGGAGAATTTCGATGAAACAAGACGACTTGTGATCTCGGTTTCAA	300
Qy	301 CCATTTAAAAGTAATTGAACCACTAGGCACCCTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301 CCATTTAAAAGTAATTGAACCACTAGGCACCCTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361 ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361 ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421 CAGGACTTCCGAAGAAATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421 CAGGACTTCCGAAGAAATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481 AATTCAACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAAGAG	540
Db	481 AATTCAACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAAGAG	540
Qy	541 CTGCCAAAGCACATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Db	541 CTGCCAAAGCACATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Qy	601 ATAGTTCTCAAATAATGACAAGCAGAAGTATACCTGCTAAATCAACCATGACTGTGTG	660
Db	601 ATAGTTCTCAAATAATGACAAGCAGAAGTATACCTGCTAAATCAACCATGACTGTGTG	660
Qy	661 CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTCTATCATCT	720
Db	661 CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTCTATCATCT	720
Qy	721 GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGTGGA	780
Db	721 GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGTGGA	780
Qy	781 TGTGATGAATACTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781 TGTGATGAATACTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Qy	841 ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	841 ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Qy	901 CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901 CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960

Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTIONGGTCAGCAGTGTGGTAAAGTCCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTIONGGTCAGCAGTGTGGTAAAGTCCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGACAGCTCAAAGCAATTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGACAGCTCAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680

Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Qy	1921	CAGGTCTAAACATATTGGATAACTTGCTGTGAGATTTTACTGAAGAAA	1980
Db	1921	CAGGTCTAAACATATTGGATAACTTGCTGTGAGATTTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTGGCATTAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGGCACTTTTCTTTGGCATTAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTCATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTCATGTGGG	2100
Qy	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTAAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2161	GACATTCTAAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCACCAGATTCTGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCACCAGATTCTGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Qy	2401	AATGAGATCATTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460

Db	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGCAATCGGTGACTGTGTGGACTTATTGAGGTGGCGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGCAATCGGTGACTGTGTGGACTTATTGAGGTGGCGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCCTGAAAGGTGACTGCAGTTAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCACTGCAAAGGCCTGAAAGGTGACTGCAGTTAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTCATGTGCTGGACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701	TTTACACGTTCATGTGCTGGACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGCCCCATTGTTTG	2880
Db	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGCCCCATTGTTTG	2880
Qy	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGTATTGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGTATTGACAGCATGCCAAT	3000
Qy	3001	CTCTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Db	3001	CTCTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Qy	3061	GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3061	GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180

Db 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240  
|||

Db 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA 3300  
|||

Db 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA 3300

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACT 3360  
|||

Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACT 3360

Qy 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTTC 3420  
|||

Db 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTTC 3420

Qy 3421 AAAA 3424  
|||

Db 3421 AAAA 3424

## RESULT 4

ADZ00490

ID ADZ00490 standard; cDNA; 3424 BP.

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AC ADZ00490;

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DT 11-JUN-2007 (revised)

DT 16-JUN-2005 (first entry)

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DE p110-beta coding sequence.

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KW ss; Anorectic; Antidiabetic; p110-beta; phosphoinositide 3-kinase; p85;

KW ras; insulin resistance; obesity; gene.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13..3219

FT /\*tag= a

XX

PN WO2005031341-A2.

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PD 07-APR-2005.

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PF 28-SEP-2004; 2004WO-IB003926.

XX

PR 29-SEP-2003; 2003US-0507226P.  
 PR 13-JUL-2004; 2004US-0587333P.

XX  
 PA (PFIZ ) PFIZER HEALTH AB.

XX  
 PI Bougneres P;

XX DR WPI; 2005-273421/28.

DR P-PSDB; ADZ00491.

DR GENBANK; Z29090.

DR PC:NCBI; gi472990.

DR PC\_ENCPRO:NCBI; gi472991.

XX  
 PT Predicting a subject's likelihood of developing insulin resistance,  
 PT useful for treating insulin resistance and obesity, comprises determining  
 PT in a subject the identity of an allele at position 100 of a specific  
 PT sequence.

XX PS Disclosure; SEQ ID NO 2; 88pp; English.

CC This sequence represents the p110-beta gene. p110-beta is a catalytic  
 CC subunit of a phosphoinositide 3-kinase, which also comprises a regulatory  
 CC subunit of about 85 kD. The p110 protein comprises a kinase domain at the  
 CC C-terminus, and a p85 and ras binding domain at the N-terminus. The  
 CC method of the invention for predicting a subject's likelihood of  
 CC developing insulin resistance comprises determining in a subject the  
 CC identity of the nucleotide present at a position corresponding to  
 CC position -359 of the p110-beta gene , where the allele comprising the  
 CC nucleotide is correlated with an increased or decreased likelihood of  
 CC developing insulin resistance. The method of the invention is useful for  
 CC treating obesity and insulin resistance and for assessing and conducting  
 CC clinical trials of medicaments.

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.

XX SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 4; Length 3424;  
 Best Local Similarity 99.9%;  
 Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGTATG 60  
 |||||||

Db 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGTATG 60

Qy 61 CCCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120  
 |||||||

Db 61 CCCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120

Qy	121	CTCCGTGAGGCATACATTAGTAACATAAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCATACATTAGTAACATAAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAAGAA	240
Qy	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Db	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Qy	301	CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCATCGCCACATGTAGAACATCTCACCAAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCATCGCCACATGTAGAACATCTCACCAAGAG	540
Qy	541	CTGCCAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGGGTGAATTGGTA	600
Db	541	CTGCCAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGGGTGAATTGGTA	600
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCAACCAGTACTGTG	660
Db	601	ATAGTTCTCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCAACCAGTACTGTG	660
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGGCTATCATCT	720
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAGTGTGGA	780
Db	721	GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAGTGTGGA	780
Qy	781	TGTGATGAATACTCCTAGAAAAATACCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTCCTAGAAAAATACCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Qy	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTAA	900
Db	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTAA	900
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Qy	1141	CCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1141	CCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTGACTGGTCAGCAGTGTGGTAAAGTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTGACTGGTCAGCAGTGTGGTAAAGTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620

Db	1561	CTAGCTAGAGACAATGAATTAGGGAAATGACAAAGAACAGCTAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGAACTATCCCCGAAATTCTACCCAAATTGCTCTGTTAAATGAAATTCT	1740
Db	1681	TATTGTGAACTATCCCCGAAATTCTACCCAAATTGCTCTGTTAAATGAAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Qy	1921	CAGGCCTAAAATATGAAACATATTGGATAACTGCTTGAGATTTCAGATGAAAGAAA	1980
Db	1921	CAGGCCTAAAATATGAAACATATTGGATAACTGCTTGAGATTTCAGATGAAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGCACTTTCTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGCACTTTCTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTGGAGTCTTATTGCTGTGAGATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTGGAGTCTTATTGCTGTGAGATGTGGG	2100
Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTAAACAGGAGAGGAAGGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2161	GACATTCTAAACAGGAGAGGAAGGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCAGCCAGATTCTATGGATGCCCTACAGGGCTTGCTGCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCAGCCAGATTCTATGGATGCCCTACAGGGCTTGCTGCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTTCTGAAAA	2340

Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGTCCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341		2400
Qy	2401	AATGAGATCATCTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Db	2401		2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGAAACATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461		2520
Qy	2521	GGTTGTCTGTCATCGTGACTGTGTGGACTTATTGAGGTGGTGCAGAATTCTCACACT	2580
Db	2521		2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGCTTGAAGAGTGCAGTCAACAGCCACACA	2640
Db	2581		2640
Qy	2641	CTACATCAGTGGCTAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641		2700
Qy	2701	TTTACACGTTCATGTGCTGGACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701		2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Db	2761		2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTTATAACGAGAACGTGTGCCATTGTTTG	2880
Db	2821		2880
Qy	2881	ACACAGGATTCTTAATAGTGTAGTAAAGGAGCCAAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881		2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT	3000
Db	2941		3000
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTT	3060
Db	3001		3060

Qy 3061 GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG 3120  
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG 3120

Qy 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180  
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240  
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300  
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360  
           |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360

Qy 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTT 3420  
           |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTT 3420

Qy 3421 AAAA 3424  
           |||||  
 Db 3421 AAAA 3424

## RESULT 5

AEH10445

ID AEH10445 standard; cDNA; 3424 BP.

XX

AC AEH10445;

XX

DT 11-JUN-2007 (revised)

DT 01-JUN-2006 (first entry)

XX

DE PIK3CA cDNA SEQ ID 831.

XX

KW gene expression; prognosis; diagnosis; DNA microarray;

KW colorectal disease; colon tumor; colorectal tumor; cytostatic;

KW gastrointestinal disease; neoplasm; ss.

XX

OS Unidentified.

XX

PN WO2005054508-A2.

XX

PD 16-JUN-2005.

XX

PF 01-DEC-2004; 2004WO-IB004323.

XX

PR 01-DEC-2003; 2003US-0525987P.

PR 01-DEC-2004; 2004US-00000688.

XX

PA (IPSO-) IPSOGEN.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (PAOL-) INST PAOLI CALMETTES IPC.

XX

PI Bertucci F, Houlgate R, Birnbaum D, Debono S;

XX

DR WPI; 2005-435408/44.

DR PC:NCBI; gi472990.

XX

PT Analyzing differential gene expression associated with histopathologic features of colorectal disease, involves detecting overexpression or underexpression of pool of polynucleotide sequences in colon tissues.

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PS Claim 1; SEQ ID NO 831; 154pp; English.

XX

CC The invention describes a method of analyzing (M1) differential gene expression associated with histopathologic features of colorectal disease, comprising detecting overexpression or underexpression of a pool of polynucleotide sequences in colon tissues, the pool selected in each of predefined polynucleotide sequence sets chosen from any one of 644 sequence sets comprising combinations of SEQ ID No. 1-1596, fully defined in the specification. Also described are: a polynucleotide library (I) useful for the molecular characterization of a colon cancer, comprising or corresponding to a pool of polynucleotide sequences either overexpressed or underexpressed in colon tissue, the pool corresponding to all or part of the polynucleotide sequence chosen from PS1; and assigning (M2) a therapeutic regimen to patient with histopathological features of colorectal disease, e.g. colon cancer, comprising classifying the patient having a poor prognosis or a good prognosis on the basis of (M1), assigning the patient a therapeutic regimen, the therapeutic regimen comprising no adjuvant chemotherapy if the patient is lymph node negative and is classified as having a good prognosis or comprising chemotherapy if the patient has any other combination of lymph node status and expression profile. (M1) is useful for analyzing differential gene expression associated with histopathologic features of colorectal disease. (M1) is useful for analyzing differential gene expression associated with colon tumors, visceral metastases in colon cancer, lymph node metastases in colon cancer, MSI phenotype in colon cancer, location of primary colorectal carcinoma, in colon cancer, and survival and death of patient in colon cancer, where the analysis comprises detection of overexpression or underexpression of pool of polynucleotide sequences in colon tissue, the pool corresponding to specific combination of

CC polynucleotide sequences from PS1, as given in the specification. (M1) is  
 CC useful for detecting, diagnosing, staging, classifying, monitoring or  
 CC predicting conditions associated with colorectal cancer. (M1) is useful  
 CC for prognosis or diagnosis or colon cancer or for monitoring the  
 CC treatment of a patient with colon cancer, which involves implementing  
 CC (M1) on nucleic acids from the patient. (M1) is useful for  
 CC differentiating a normal cell from a cancer cell, which involves  
 CC implementing (M1) on nucleic acids from the cells. (M1) is useful for  
 CC selecting appropriate doses and/or schedule of chemotherapeutics and/or  
 CC (bio)pharmaceuticals and/or target agents e.g. Irinotecan, 5-fluorouracil  
 CC and methotrexate. This sequence represents a polynucleotide identified in  
 CC the analysis of differential gene expression associated with  
 CC histopathological features of colorectal disease. Note: The sequence data  
 CC for this patent is not represented in the printed specification but is  
 CC based on sequence information supplied by the European Patent Office.  
 CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
 CC information from BOND.

XX

SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 4; Length 3424;  
 Best Local Similarity 99.9%;  
 Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGTATG 60
Db	1 AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGTATG 60
Qy	61 CCCCAAGAATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
Db	61 CCCCAAGAATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC 120
Qy	121 CCTCGTAGGCTACATTAGTAACATAAACGATGAACATTAAAGAAGCAAGAAAATAC 180
Db	121 CCTCGTAGGCTACATTAGTAACATAAACGATGAACATTAAAGAAGCAAGAAAATAC 180
Qy	181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAGAA 240
Db	181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAGAA 240
Qy	241 GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA 300
Db	241 GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA 300
Qy	301 CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360
Db	301 CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360

Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTCCGAAGAAATATTCTTAATGTTGAAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTCCGAAGAAATATTCTTAATGTTGAAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTACACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACAGAG	540
Db	481	AATTACACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCAAATAATAGTGGTGAATTGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCAAATAATAGTGGTGAATTGGTA	600
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTCTATCATCT	720
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTCTATCATCT	720
Qy	721	GAACAAATTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Db	721	GAACAAATTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAATATCCTCTGAGTCAGTATAAGTATAAGAACGCTGT	840
Db	781	TGTGATGAATACTTCCTAGAAAATATCCTCTGAGTCAGTATAAGTATAAGAACGCTGT	840
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140

Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTTCATCCAGTGGAAATGGAATGGCTGAATTATGATATACATTCTGTACCTT	1200
Db	1141	CCTTGTTCATCCAGTGGAAATGGAATGGCTGAATTATGATATACATTCTGTACCTT	1200
Qy	1201	CCTCGTGTCTCGACTTGCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTCTCGACTTGCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGAUTGGTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGAUTGGTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAACGCAGGATTAGCTATTCCCACGCAGGACTGAGAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAACGCAGGATTAGCTATTCCCACGCAGGACTGAGAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAGGAAATGACAAAGAACAGCTAAAGCAATTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAGGAAATGACAAAGAACAGCTAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGCTGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCAAACACTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCAAACACTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCTATGGTCGAGGTTTGTGTT	1860

Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAAATATTAACAGATGACAAACTTCTCAGTATTAATTCACTGAGTAGTA	1920
Db	1861	CGGTGCTTGGAAAAAATATTAACAGATGACAAACTTCTCAGTATTAATTCACTGAGTAGTA	1920
Qy	1921	CAGGTCTAAATATGAACAATATTGGATAACTGCTGTGAGATTTACTGAAGAAA	1980
Db	1921	CAGGTCTAAATATGAACAATATTGGATAACTGCTGTGAGATTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAACAGGATTGGGCACTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAACAGGATTGGGCACTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCTGCTTTGGAGTCCTATTGCGATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCTGCTTTGGAGTCCTATTGCGATGTGGG	2100
Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTCAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2161	GACATTCTCAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTCTAGGGATGCCCTACAGGGCTGCTGCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCGACCAGATTCTAGGGATGCCCTACAGGGCTGCTGCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTAGAAC	2400
Db	2341	AGGCCACTGTGGTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTAGAAC	2400
Qy	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Db	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGAAACATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGGAAAATATCTGGAAACATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGTCATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGTCATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580

Qy	2581	ATTATGCAAATTCACTGCAAAGCGGTTGAAAGGTGCACTGCAGTCAACAGCCACACA	2640
Db	2581		
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641		
Qy	2701	TTTACACGTTCATGTGCTGGACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701		
Qy	2761	CACAATAGTAACATCATGGTGAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Db	2761		
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTTATAACGAGAACGTGTGCCATTGTTTG	2880
Db	2821		
Qy	2881	ACACAGGATTCTTAATAGTGTGATTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881		
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT	3000
Db	2941		
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTT	3060
Db	3001		
Qy	3061	GATGACATTGCATACATCGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3061		
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121		
Qy	3181	TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181		
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA	3300
Db	3241		

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360  
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360

Qy 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTC 3420  
   ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTC 3420

Qy 3421 AAAA 3424  
   ||||  
 Db 3421 AAAA 3424

## RESULT 6

AED31618

ID AED31618 standard; cDNA; 3424 BP.

XX

AC AED31618;

XX

DT 15-DEC-2005 (first entry)

XX

DE cDNA (SEQ ID No:2) encoding human phosphatidylinositol 3-kinase (PIK3CA).

XX

KW cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;

KW chemotherapy; cytostatic; RNA interference; gene silencing;

KW antisense therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 13. .3219

FT /\*tag= a

FT /product= "PIK3CA"

XX

PN WO2005091849-A2.

XX

PD 06-OCT-2005.

XX

PF 18-FEB-2005; 2005WO-US005193.

XX

PR 02-MAR-2004; 2004US-0548886P.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;

XX

DR WPI; 2005-713721/73.

DR P-PSDB; AED31619.

XX

PT Assessing cancer in a human suspected of having cancer, by determining a  
 PT non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase  
 PT (PIK3CA) coding sequence in the body sample from a human.

XX  
 PS Claim 1; SEQ ID NO 2; 107pp; English.  
 XX

CC The invention relates to a method of assessing cancer in a body sample of  
 CC a human suspected of having cancer. The method comprises determining a  
 CC non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase  
 CC (PIK3CA) coding sequence in the body sample, and identifying the human as  
 CC likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA  
 CC coding sequence is determined in the body sample. Also described are: (1)  
 CC a method of inhibiting progression of a tumor in a human; (2) a method of  
 CC identifying candidate chemotherapeutic agents; (3) a method for  
 CC delivering an appropriate chemotherapeutic drug to a patient in need; and  
 CC (4) a set of one or more primers for amplifying and/or sequencing PIK3CA,  
 CC the primers selected from forward primers, reverse primers, or sequencing  
 CC primers, where the forward primers are selected from sequences given as  
 CC SEQ ID NOS 6-165, the reverse primers are selected from sequences given  
 CC as SEQ ID NOS 166-325, and the sequencing primers are selected sequences  
 CC given as SEQ ID NOS 326-485 in the specification. The method of the  
 CC invention is useful for assessing cancer in a body sample of a human  
 CC suspected of having cancer, inhibiting progression of a tumor in a human,  
 CC identifying candidate chemotherapeutic agents, and delivering an  
 CC appropriate chemotherapeutic drug to a patient in need. This sequence  
 CC encodes human PIK3CA.

XX  
 SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match 99.9%; Score 3422.4; DB 4; Length 3424;  
 Best Local Similarity 99.9%;  
 Matches 3423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 60  
 |||||||

Db 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 60

Qy 61 CCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATACTGACTTTAGAATGC 120  
 |||||||

Db 61 CCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATACTGACTTTAGAATGC 120

Qy 121 CCTCGTGAGGCATCACATTAGTAACATATAAGCATGAACATTAAAGAAGCAAGAAAATAC 180  
 |||||||

Db 121 CCTCGTGAGGCATCACATTAGTAACATATAAGCATGAACATTAAAGAAGCAAGAAAATAC 180

Qy 181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAGAA 240  
 |||||||

Db 181 CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAGAA 240

Qy	241	GCAGAAAGGGAGAATTGATGAAACAAGACGACTTGTGATCTCGGTTTC 300 
Db	241	GCAGAAAGGGAGAATTGATGAAACAAGACGACTTGTGATCTCGGTTTC 300 
Qy	301	CCATTTAAAAGTAATTGACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360 
Db	301	CCATTTAAAAGTAATTGACCAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA 360 
Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA 420 
Db	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA 420 
Qy	421	CAGGACTCCGAAGAAATATTCTAACATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT 480 
Db	421	CAGGACTCCGAAGAAATATTCTAACATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT 480 
Qy	481	AATTACACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAAGAG 540 
Db	481	AATTACACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAAGAG 540 
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA 600 
Db	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA 600 
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTG 660 
Db	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTG 660 
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT 720 
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT 720 
Qy	721	GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA 780 
Db	721	GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA 780 
Qy	781	TGTGATGAATACTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT 840 
Db	781	TGTGATGAATACTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT 840 
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA 900 
Db	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA 900 
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA 960 
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA 960 
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAATAGAGCACTCAGAATA 1020 

Db	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAATATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTTGACTGGTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAACAGATTTCATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAACAGATTTCATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGGAATTCT	1740

Db	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741		
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCATGGTCGAGGTTTGCTGTT	1860
Db	1801		
Db	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAAATATTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTA	1920
Db	1861		
Db	1861	CGGTGCTTGGAAAAAATATTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTA	1920
Qy	1921	CAGGTCTAAATATGAACAAATTGGATAACTTGCTTGTGAGATTTACTGAAGAAA	1980
Db	1921		
Db	1921	CAGGTCTAAATATGAACAAATTGGATAACTTGCTTGTGAGATTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAACAGGATGGGACTTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Db	1981		
Db	1981	GCATTGACTAACAGGATGGGACTTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTCATGTGGG	2100
Db	2041		
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTCATGTGGG	2100
Qy	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101		
Db	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTGTAGTT	2220
Db	2161		
Db	2161	GACATTCTAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTGTAGTT	2220
Qy	2221	GAGCAAATGAGGCGACCAGATTCTAGGGATGCCCTACAGGGCTGCTGTCCTCTAAAC	2280
Db	2221		
Db	2221	GAGCAAATGAGGCGACCAGATTCTAGGGATGCCCTACAGGGCTGCTGTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Db	2281		
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTAGAAC	2400
Db	2341		
Db	2341	AGGCCACTGTGGTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTAGAAC	2400
Qy	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Db	2401		
Db	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460

Qy	2461	ATTCGTATTATGGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461		2520
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTTGGACTTATTGAGGTGGTGCAGAATTCTCACACT	2580
Db	2521		2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCCGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2640
Db	2581		2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2641		2700
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701		2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Db	2761		2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTATACGAGAACGTGTGCCATTGTTTG	2880
Db	2821		2880
Qy	2881	ACACAGGATTCTTAATAGTGAATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881		2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT	3000
Db	2941		3000
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAATCTTT	3060
Db	3001		3060
Qy	3061	GATGACATTGCATACATCGAAAGACCCTAGCCTAGATAAAAACTGAGCAAGAGGCTTG	3120
Db	3061		3120
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121		3180

Qy 3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA 3300  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGAAAGACCGATTGCA 3300

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360  
           ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360

Qy 3361 ATATAATTAAATAATGTAAACGCACAGGGTTGATAGCACTTAAACTAGTTCATTT 3420  
           ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3361 ATATAATTAAATAATGTAAACGCACAGGGTTGATAGCACTTAAACTAGTTCATTT 3420

Qy 3421 AAAA 3424  
           ||||  
 Db 3421 AAAA 3424

## RESULT 7

AEG93388

ID AEG93388 standard; cDNA; 3424 BP.

XX

AC AEG93388;

XX

DT 11-JUN-2007 (revised)

DT 01-JUN-2006 (first entry)

XX

DE Human tumor cell cDNA SEQ ID NO:884.

XX

KW Gene expression; tumor; ss.

XX

OS Homo sapiens.

XX

PN WO2006036025-A1.

XX

PD 06-APR-2006.

XX

PF 30-SEP-2005; 2005WO-JP018574.

XX

PR 30-SEP-2004; 2004JP-00286259.

PR 28-FEB-2005; 2005JP-00054475.

PR 28-FEB-2005; 2005JP-00054866.

XX

PA (EISA ) EISAI CO LTD.

XX

PI Owa T, Yokoi A, Ozawa Y, Kawai T, Ushijima R;

XX

DR WPI; 2006-293404/30.

DR PC:NCBI; gi472990.

DR PC\_ENCPRO:NCBI; gi472991.

XX

PT Evaluating sensitivity of a tumor cell to a sulfonamide-containing compound, comprises comparing the expression of specific genes in tumor cells before and after administration of the compound.

XX

PS Claim 1; SEQ ID NO 884; 1405pp; Japanese.

XX

CC The invention relates to a method of evaluating the sensitivity of a tumor cell to a sulfonamide-containing compound, by comparing the expression level of genes in tumor cells obtained from cancer patients before and after administration of the sulfonamide-containing compound and determining the tumor cell to be sensitive to the sulfonamide-containing compound, when the expression amount of genes in the cell is increased compared with the expression amount before administration and/or when the expression amount of one or more genes is decreased compared with the expression amount before administration. The invention also relates to an assay reagent of RNA comprising an oligonucleotide complementary to an RNA which is the transcription product of a gene, and an immunoassay reagent containing the antibody with respect to a protein which is a translation product of the gene. The expression level of the gene, which is the RNA transcription product, is measured using a DNA microarray or by quantitative PCR. The expression level of protein, which is a translation product of the gene, is measured by an immunochemical method such as enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) or Western blotting. The method enables evaluation of the sensitivity of a tumor cell to a sulfonamide-containing compound. This sequence represents human tumor cell cDNA used in the scope of the invention.

CC

CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed information from BOND.

XX

SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 U; 0 Other;

Query Match	99.9%	Score	3422.4	DB	4	Length	3424		
Best Local Similarity	99.9%								
Matches	3423	Conservative	0	Mismatches	1	Indels	0	Gaps	0

Qy

1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGA	ACTGTGGGGCATCCACTTGTATG	60

Db

1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGA	ACTGTGGGGCATCCACTTGTATG	60

Qy

61	CCCCAAGAACCTAGTGGATGTTACTACCAATGGA	ATGATGAGTGTACTTTAGAATGC	120

Db

61	CCCCAAGAACCTAGTGGATGTTACTACCAATGGA	ATGATGAGTGTACTTTAGAATGC	120

Qy	121	CTCCGTGAGGCATACATTAGTAACATAAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCATACATTAGTAACATAAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAAGAA	240
Db	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAAGAA	240
Qy	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Db	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Qy	301	CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCATCCGCCACATGTAGAACATCTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCATCCGCCACATGTAGAACATCTCACCAGAG	540
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGGGTGAATTGGTA	600
Db	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGGGTGAATTGGTA	600
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCAACCATGACTGTG	660
Db	601	ATAGTTCTCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCAACCATGACTGTG	660
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGGCTATCATCT	720
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGGCTATCATCT	720
Qy	721	GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAGTGTG	780
Db	721	GAACAATTAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAGTGTG	780
Qy	781	TGTGATGAATACTCCTAGAAAAATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	781	TGTGATGAATACTCCTAGAAAAATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840

Qy	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTAA	900
Db	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTAA	900
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTGACTGGTCAGCAGTGTGGTAAAGTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	TTGACTGGTCAGCAGTGTGGTAAAGTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620

Db	1561	CTAGCTAGAGACAATGAATTAGGGAAATGACAAAGAACAGCTAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGAAATTCT	1740
Db	1681	TATTGTGAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGAAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTCACTAGTAGTA	1920
Qy	1921	CAGGCCTAAAATATGAACAATATTGGATAACTGCTTGAGATTTCAGACTGAGAAA	1980
Db	1921	CAGGCCTAAAATATGAACAATATTGGATAACTGCTTGAGATTTCAGACTGAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGCACTTTCTTTGGCATTTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGCACTTTCTTTGGCATTTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCTGTGATGTGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCTGTGATGTGGG	2100
Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAAGCTCATTAACCTAACT	2160
Db	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAAGCTCATTAACCTAACT	2160
Qy	2161	GACATTCTAAACAGGAGAGGAAGGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2161	GACATTCTAAACAGGAGAGGAAGGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCAGCCAGATTCTATGGATGCCCTACAGGGCTTGCTGTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCAGCCAGATTCTATGGATGCCCTACAGGGCTTGCTGTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTTCTGAAAA	2340

Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGTCCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAGAAC	2400
Db	2341		2400
Qy	2401	AATGAGATCATCTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Db	2401		2460
Qy	2461	ATTCGTATTATGGAAAATATCTGGAAACATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461		2520
Qy	2521	GGTTGTCTGTCATCGTGACTGTGTGGACTTATTGAGGTGGTGCAGAATTCTCACACT	2580
Db	2521		2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTAACAGCCACACA	2640
Db	2581		2640
Qy	2641	CTACATCAGTGGCTAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG	2700
Db	2641		2700
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701		2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Db	2761		2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGTGCCATTGTTTG	2880
Db	2821		2880
Qy	2881	ACACAGGATTCTTAATAGTGTAGTAAAGGAGCCAAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881		2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGTATTGACAGCATGCCAAT	3000
Db	2941		3000
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTT	3060
Db	3001		3060

Qy 3061 GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG 3120  
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 GATGACATTGCATACATCGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG 3120

Qy 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180  
       ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240  
       ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA 3240

Qy 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300  
       ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA 3300

Qy 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360  
       ||||||||||||||||||||||||||||||||||||||||  
 Db 3301 TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAATACT 3360

Qy 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTT 3420  
       ||||||||||||||||||||||||||||||||||||||||  
 Db 3361 ATATAATTAAATAATGTAAACGCAAACAGGGTTTGATAGCACTTAAACTAGTTCATTT 3420

Qy 3421 AAAA 3424  
       ||||  
 Db 3421 AAAA 3424

## RESULT 8

AAQ51156

ID AAQ51156 standard; cDNA; 3412 BP.

XX

AC AAQ51156;

XX

DT 25-MAR-2003 (revised)

DT 12-APR-1994 (first entry)

XX

DE Human p110 cDNA.

XX

KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist;  
 KW cell proliferation; inhibition; prophylaxis; therapy; platelets;  
 KW neutrophil activity; 3-phosphorylated phosphoinositides; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers  
 FT CDS 1..3207

FT                           /\*tag= a  
 FT                           /note= "PI3- kinase p110"  
 XX  
 PN WO9321328-A1.  
 XX  
 PD 28-OCT-1993.  
 XX  
 PF 13-APR-1993; 93WO-GB000761.  
 XX  
 PR 13-APR-1992; 92GB-00008135.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;  
 PI Panayotou G, Volinia S, Gout I;  
 XX  
 DR WPI; 1993-351738/44.  
 DR P-PSDB; AAR43342.  
 XX  
 PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase activity,  
 PT useful for controlling cell proliferation.  
 XX  
 PS Claim 7; Fig 16; 146pp; English.  
 XX  
 CC Southern blot analysis was performed using a bovine cDNA probe contg. a  
 CC fragment of a PI3-kinase-encoding sequence and human cDNA isolated from a  
 CC cDNA library constructed from mRNA isolated from the human cell line  
 CC KG1a. Positive clones were sequenced to give the human PI3 kinase p110  
 CC sequence shown. This sequence has 95 percent homology with the bovine  
 CC sequence. The domain encoding residues 19- 100 of human p110 is  
 CC sufficient to encode the kinase which will associate with the p85 kinase  
 CC subunit. The gene may be used to provide a protein with PI3 kinase  
 CC activity, and is useful for screening for (ant)agonists of PI3 kinase  
 CC activity which could be useful for stimulation or inhibition of cell  
 CC proliferation and hence prophylaxis or therapy. Platelet or neutrophil  
 CC activity or blood glucose levels can be controlled using the kinase. See  
 CC also AAQ51155 and AAQ57522-3. (Updated on 25-MAR-2003 to correct PN  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

Query Match               99.6%; Score 3410.4; DB 1; Length 3412;  
 Best Local Similarity   99.9%;  
 Matches 3411; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy                        13 ATGCCTCCAAGACCATCATCAGGTGAACGTGGGGATCCACTTGATCCCCCAAGAAC 72  
                           |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db                        1 ATGCCTCCAAGACCATCATCAGGTGAACGTGGGGATCCACTTGATCCCCCAAGAAC 60

Qy	73	CTAGTGGAAATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	132
Db	61	CTAGTGGAAATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGCCTCCGTGAGGCT	120
Qy	133	ACATTAGTAACATAAAGCATGAACATTAAAGAAGCAAGAAAATACCCTCTCCATCAA	192
Db	121	ACATTAGTAACATAAAGCATGAACATTAAAGAAGCAAGAAAATACCCTCTCCATCAA	180
Qy	193	CTTCTTCAGATGAATCTCTTACATTTCTGAAGTGTACCCAGAACAGCAGAAAGGGAA	252
Db	181	CTTCTTCAGATGAATCTCTTACATTTCTGAAGTGTACCCAGAACAGCAGAAAGGGAA	240
Qy	253	GAATTTTTGATGAAACAAGACGACTTTGTGATCTCGGCTTTTCAACCATTAAAAAA	312
Db	241	GAATTTTTGATGAAACAAGACGACTTTGTGATCTCGGCTTTTCAACCATTAAAAAA	300
Qy	313	GTAATTGAAACCACTAGGCAACCGTAGGAAAGAACATCCTCAATCGAGAAAATTGGTTGCT	372
Db	301	GTAATTGAAACCACTAGGCAACCGTAGGAAAGAACATCCTCAATCGAGAAAATTGGTTGCT	360
Qy	373	ATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTACAGGACTTCCGA	432
Db	361	ATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTACAGGACTTCCGA	420
Qy	433	AGAAATATTCTTAATGTTGAAAGAACGCTGTGGATCTAGGGATCTTAATTCACCTCAT	492
Db	421	AGAAATATTCTTAATGTTGAAAGAACGCTGTGGATCTAGGGATCTTAATTCACCTCAT	480
Qy	493	AGTAGAGCAATGTATGCTATCCGCCACATGTAGAATCTCACAGAGCTGCCAAGCAC	552
Db	481	AGTAGAGCAATGTATGCTATCCGCCACATGTAGAATCTCACAGAGCTGCCAAGCAC	540
Qy	553	ATATATAATAATTGGATAGAGGCCAATAATAGTGGTATTGGTAATAGTTCTCCA	612
Db	541	ATATATAATAATTGGATAGAGGCCAATAATAGTGGTATTGGTAATAGTTCTCCA	600
Qy	613	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGCCAGAACAGTA	672
Db	601	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGCCAGAACAGTA	660
Qy	673	ATTGCTGAAGCAATCAGGAAAAAAACTAGAACGATGTTGCTATCATCTGAACATTAAAA	732
Db	661	ATTGCTGAAGCAATCAGGAAAAAAACTAGAACGATGTTGCTATCATCTGAACATTAAAA	720
Qy	733	CTCTGTGTTTGAATATCAGGGCAAGTACATTTAAAAGTGTGGATGTGATGAATAC	792
Db	721	CTCTGTGTTTGAATATCAGGGCAAGTACATTTAAAAGTGTGGATGTGATGAATAC	780
Qy	793	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATAAGAACAGCTGTATAATGCTGGG	852

Db	781	TTCTAGAAAAATATCCTGAGTCAGTATAAGTATAAGAAGCTATAATGCTGGG	840
Qy	853	AGGATGCCAATTGAAAGATGATGGCTAAAGAACGCTTATTCTCACTGCCAATGGAC	912
Db	841	AGGATGCCAATTGAAAGATGATGGCTAAAGAACGCTTATTCTCACTGCCAATGGAC	900
Qy	913	TGTTTACAATGCCATCTATTCCAGACGCATTCCACAGCTACACCATATATGAATGGA	972
Db	901	TGTTTACAATGCCATCTATTCCAGACGCATTCCACAGCTACACCATATATGAATGGA	960
Qy	973	GAAACATCTACAAAATCCCTTGGGTATAAATAGACTCAGAATAAAAATTCTTGT	1032
Db	961	GAAACATCTACAAAATCCCTTGGGTATAAATAGACTCAGAATAAAAATTCTTGT	1020
Qy	1033	GCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTCGAACAGGTATC	1092
Db	1021	GCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTCGAACAGGTATC	1080
Qy	1093	TACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGTACCTGTCAT	1152
Db	1081	TACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGTACCTGTCAT	1140
Qy	1153	CCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTCCTCGTGTGCT	1212
Db	1141	CCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTCCTCGTGTGCT	1200
Qy	1213	CGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTCTAAAGAGGAACACTGT	1272
Db	1201	CGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTCTAAAGAGGAACACTGT	1260
Qy	1273	CCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTAGTATCTGGAAAA	1332
Db	1261	CCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTAGTATCTGGAAAA	1320
Qy	1333	ATGGCTTGAAATTTGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1392
Db	1321	ATGGCTTGAAATTTGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1380
Qy	1393	GTTACTGGATCAAATCCAATAAGAACCTCCATGCTTAGAGTTGGAGTTGACTGGTC	1452
Db	1381	GTTACTGGATCAAATCCAATAAGAACCTCCATGCTTAGAGTTGGAGTTGACTGGTC	1440
Qy	1453	AGCAGTGTGTAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGCTGTA	1512
Db	1441	AGCAGTGTGTAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGCTGTA	1500
Qy	1513	TCCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1572

Db	1501	TCCCGAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1560
Qy	1573	AATGAATTAAAGGGAAAATGACAAAGAACAGCTCAAGCAATTCTACACGAAATCCTCTC	1632
Db	1561	AATGAATTAAAGGGAAAATGACAAAGAACAGCTCAAGCAATTCTACACGAGATCCTCTC	1620
Qy	1633	TCTGAAATCACTGAGCAGGAGAAAGATTTCTATGGAGTCACAGACACTATTGTGTAAC	1692
Db	1621	TCTGAAATCACTGAGCAGGAGAAAGATTTCTATGGAGTCACAGACACTATTGTGTAAC	1680
Qy	1693	ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGAAATTCTAGAGATGAAGTA	1752
Db	1681	ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGAAATTCTAGAGATGAAGTA	1740
Qy	1753	GCCCAGATGTATTGCTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1812
Db	1741	GCCCAGATGTATTGCTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1800
Qy	1813	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGCTGTTGGTCTGGAA	1872
Db	1801	CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGCTGTTGGTCTGGAA	1860
Qy	1873	AAATATTAACAGATGACAAACTTCTCAGTATTAATTCACTAGTAGTACAGGTCTAAAA	1932
Db	1861	AAATATTAACAGATGACAAACTTCTCAGTATTAATTCACTAGTAGTACAGGTCTAAAA	1920
Qy	1933	TATGAACAATATTGGATAACCTGCTTGTGAGATTTTACTGAAGAAAGCATGACTAAT	1992
Db	1921	TATGAACAATATTGGATAACCTGCTTGTGAGATTTTACTGAAGAAAGCATGACTAAT	1980
Qy	1993	CAAAGGATTGGGCACTTTCTTTGGCATTTAAATCTGAGATGCCACAATAAACAGTT	2052
Db	1981	CAAAGGATTGGGCACTTTCTTTGGCATTTAAATCTGAGATGCCACAATAAACAGTT	2040
Qy	2053	AGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTGAAG	2112
Db	2041	AGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTGAAG	2100
Qy	2113	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTATTAACCTAACATCTCAAA	2172
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTATTAACCTAACATCTCAAA	2160
Qy	2173	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTTGAGCAAATGAGG	2232
Db	2161	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTTGAGCAAATGAGG	2220
Qy	2233	CGACCAGATTTCATGGATGCCCTACAGGGCTGCTGTCCTCTAAACCTGCTCATCAA	2292
Db	2221	CGACCAGATTTCATGGATGCCCTACAGGGCTGCTGTCCTCTAAACCTGCTCATCAA	2280

Qy	2293	CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTTCTGC 	2352
Db	2281	CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTTCTGC 	2340
Qy	2353	TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTT 	2412
Db	2341	TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTT 	2400
Qy	2413	TTAAAAATGGGGATGATTACGGCAAGATATGCTAACACT 	2472
Db	2401	TTAAAAATGGGGATGATTACGGCAAGATATGCTAACACT 	2460
Qy	2473	GAAAATATCTGGCAAAATCAAGGTCTGATCTCGAATGTT 	2532
Db	2461	GAAAATATCTGGCAAAATCAAGGTCTGATCTCGAATGTT 	2520
Qy	2533	ATCGGTGACTGTGTTGGACTTATTGAGGGTGTGCG 	2592
Db	2521	ATCGGTGACTGTGTTGGACTTATTGAGGGTGTGCG 	2580
Qy	2593	CAGTGCAAAGGCGGCTTGAAGGTGCACTGCAG 	2652
Db	2581	CAGTGCAAAGGCGGCTTGAAGGTGCACTGCAG 	2640
Qy	2653	CTCAAAGACAAGAACAAAGGAGAAATATGATG 	2712
Db	2641	CTCAAAGACAAGAACAAAGGAGAAATATGATG 	2700
Qy	2713	TGTGCTGGATACTGTGAGCTACCTCATTGG 	2772
Db	2701	TGTGCTGGATACTGTGAGCTACCTCATTGG 	2760
Qy	2773	ATCATGGTAAAGACGATGGACA 	2832
Db	2761	ATCATGGTAAAGACGATGGACA 	2820
Qy	2833	AAGAAGAAAAATTGGTTATAAACGAGAAC 	2892
Db	2821	AAGAAGAAAAATTGGTTATAAACGAGAAC 	2880
Qy	2893	TTAATAGTAGTAAAGGAGCC 	2952
Db	2881	TTAATAGTAGTAAAGGAGCC 	2940
Qy	2953	CAGGAGATGTGTTACAAGGCTTATCTAG 	3012
Db	2941	CAGGAGATGTGTTACAAGGCTTATCTAG 	3000

Qy	3013	CTTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTGATGACATTGCA	3072
Db	3001	CTTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTGATGACATTGCA	3060
Qy	3073	TACATTGAAAGACCCTAGCCTTAGATAAAAAGTGAAGCAAGAGGCTTGGAGTATTCATG	3132
Db	3061	TACATTGAAAGACCCTAGCCTTAGATAAAAAGTGAAGCAAGAGGCTTGGAGTATTCATG	3120
Qy	3133	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTCCAC	3192
Db	3121	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTCCAC	3180
Qy	3193	ACAATTAAACAGCATGCACTGAAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3252
Db	3181	ACAATTAAACAGCATGCACTGAAACTGAAAGATAACTGAGAAAATGAAAGCTCACTCTGGA	3240
Qy	3253	TTCCACACTGCACTGTTAATAACTCTCACAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3312
Db	3241	TTCCACACTGCACTGTTAATAACTCTCACAGCAGGCAAAGACCGATTGCATAGGAATTGCAC	3300
Qy	3313	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAACTATATAATTAAA	3372
Db	3301	AATCCATGAACAGCATTAGATTTACAGCAAGAACAGAAATAAAACTATATAATTAAA	3360
Qy	3373	TAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATTCAAAA	3424
Db	3361	TAATGTAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATTCAAAA	3412

## RESULT 9

AED31617

ID AED31617 standard; cDNA; 3412 BP.

XX

AC AED31617;

XX

DT 15-DEC-2005 (first entry)

XX

DE cDNA (SEQ ID No:1) encoding human phosphatidylinositol 3-kinase (PIK3CA).

XX

KW cancer; neoplasm; phosphatidylinositol 3-kinase; PIK3CA; tumor;  
KW chemotherapy; cytostatic; RNA interference; gene silencing;  
KW antisense therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1..3207
FT		/*tag= a
FT		/product= "PIK3CA"

XX  
 PN WO2005091849-A2.

XX  
 PD 06-OCT-2005.

XX  
 PF 18-FEB-2005; 2005WO-US005193.

XX  
 PR 02-MAR-2004; 2004US-0548886P.

XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.

XX  
 PI Samuels Y, Velculescu V, Kinzler KW, Vogelstein B;

XX  
 DR WPI; 2005-713721/73.  
 DR P-PSDB; AED31619.

XX  
 PT Assessing cancer in a human suspected of having cancer, by determining a non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase (PIK3CA) coding sequence in the body sample from a human.

XX  
 PS Disclosure; SEQ ID NO 1; 107pp; English.

CC The invention relates to a method of assessing cancer in a body sample of a human suspected of having cancer. The method comprises determining a non-synonymous, intragenic mutation in a phosphatidylinositol 3-kinase (PIK3CA) coding sequence in the body sample, and identifying the human as likely to have cancer if a non-synonymous, intragenic mutation in PIK3CA coding sequence is determined in the body sample. Also described are: (1) a method of inhibiting progression of a tumor in a human; (2) a method of identifying candidate chemotherapeutic agents; (3) a method for delivering an appropriate chemotherapeutic drug to a patient in need; and (4) a set of one or more primers for amplifying and/or sequencing PIK3CA, the primers selected from forward primers, reverse primers, or sequencing primers, where the forward primers are selected from sequences given as SEQ ID NOS 6-165, the reverse primers are selected from sequences given as SEQ ID NOS 166-325, and the sequencing primers are selected sequences given as SEQ ID NOS 326-485 in the specification. The method of the invention is useful for assessing cancer in a body sample of a human suspected of having cancer, inhibiting progression of a tumor in a human, identifying candidate chemotherapeutic agents, and delivering an appropriate chemotherapeutic drug to a patient in need. This sequence encodes human PIK3CA.

XX  
 SQ Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 U; 0 Other;

Query Match	99.6%	Score	3410.4	DB	4	Length	3412
Best Local Similarity	99.9%						
Matches	3411	Conservative	0	Mismatches	1	Indels	0
						Gaps	0

Qy	13	ATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGCATCCACTTGATGCCCAAGAAC 72 
Db	1	ATGCCTCCAAGACCATCATCAGGTGAAGTGTGGGCATCCACTTGATGCCCAAGAAC 60
Qy	73	CTAGTGGATTTACTACCAAATGGAATGATAGTGACTTAGAATGCCCTCCGTGAGGCT 132 
Db	61	CTAGTGGATTTACTACCAAATGGAATGATAGTGACTTAGAATGCCCTCCGTGAGGCT 120
Qy	133	ACATTAGTAACATAAAGCATGAACTATTAAAGAAGCAAGAAAATCCCTCTCCATCAA 192 
Db	121	ACATTAGTAACATAAAGCATGAACTATTAAAGAAGCAAGAAAATCCCTCTCCATCAA 180
Qy	193	CTTCTTCAGATGAATCTTACATTTCTGTAAGTGTACCCAGAACAGCAGAAAGGAA 252 
Db	181	CTTCTTCAGATGAATCTTACATTTCTGTAAGTGTACCCAGAACAGCAGAAAGGAA 240
Qy	253	GAATTTTGATGAAACAAGACGACTTGTGATCTCGCTTTCAACCATTAAAAA 312 
Db	241	GAATTTTGATGAAACAAGACGACTTGTGATCTCGCTTTCAACCATTAAAAA 300
Qy	313	GTAATTGAAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTGCT 372 
Db	301	GTAATTGAAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAAATTGGTTGCT 360
Qy	373	ATCGGCATGCCAGTGTGCAATTGATATGGTAAAGATCCTGAAGTACAGGACTCCGA 432 
Db	361	ATCGGCATGCCAGTGTGCAATTGATATGGTAAAGATCCTGAAGTACAGGACTCCGA 420
Qy	433	AGAAATATTCTTAATGTTGTAAGAACAGCTGTGGATCTAGGGATCTAATTCACTCAT 492 
Db	421	AGAAATATTCTTAATGTTGTAAGAACAGCTGTGGATCTAGGGATCTAATTCACTCAT 480
Qy	493	AGTAGAGCAATGTATGCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC 552 
Db	481	AGTAGAGCAATGTATGCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCAC 540
Qy	553	ATATATAATAATTGGATAGAGGCCAATAATAGTGGTATTGGTAATAGTTCTCCA 612 
Db	541	ATATATAATAATTGGATAGAGGCCAATAATAGTGGTATTGGTAATAGTTCTCCA 600
Qy	613	AATAATGACAAGCAGAAGTACTCTGAAAATCAACCATGACTGTGTGCCAGAACAGTA 672 
Db	601	AATAATGACAAGCAGAAGTACTCTGAAAATCAACCATGACTGTGTGCCAGAACAGTA 660
Qy	673	ATTGCTGAAGCAATCAGGAAAAAAACTAGAACAGTATGTTGCTATCATCTGAACAATTAAAAA 732 
Db	661	ATTGCTGAAGCAATCAGGAAAAAAACTAGAACAGTATGTTGCTATCATCTGAACAATTAAAAA 720
Qy	733	CCTGTGTTTAGAATATCAGGGCAAGTACATTAAAAGTGTGTGGATGTGATGAATAC 792

Db	721	CTCTGTGTTAGAATATCAGGGCAAGTACATTAAAAGTGTGGATGTGAATACT	780
Qy	793	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTGGG	852
Db	781	TTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTGGG	840
Qy	853	AGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCACTGCCAATGGAC	912
Db	841	AGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCACTGCCAATGGAC	900
Qy	913	TGTTTACAATGCCATCTTATTCCAGCAGCATTCCACAGCTACACCATAATGAATGGA	972
Db	901	TGTTTACAATGCCATCTTATTCCAGCAGCATTCCACAGCTACACCATAATGAATGGA	960
Qy	973	GAAACATCTACAAAATCCCTTGGTTATAAATAGAGCACTCAGAATAAAAATTCTTG	1032
Db	961	GAAACATCTACAAAATCCCTTGGTTATAAATAGAGCACTCAGAATAAAAATTCTTG	1020
Qy	1033	GCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTTATGTCGAACAGGTATC	1092
Db	1021	GCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTTATGTCGAACAGGTATC	1080
Qy	1093	TACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTACCTGTTCAAT	1152
Db	1081	TACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTACCTGTTCAAT	1140
Qy	1153	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCGTATCTCGTGTGCT	1212
Db	1141	CCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCCGTATCTCGTGTGCT	1200
Qy	1213	CGACTTGCCTTCCATTGCTCTGTTAAAGGCCAACGGGTGCTAAAGAGGAACACTGT	1272
Db	1201	CGACTTGCCTTCCATTGCTCTGTTAAAGGCCAACGGGTGCTAAAGAGGAACACTGT	1260
Qy	1273	CCATTGGCATGGGAAATATAAACTGTTGATTACACAGACACTCTAGTATCTGGAAA	1332
Db	1261	CCATTGGCATGGGAAATATAAACTGTTGATTACACAGACACTCTAGTATCTGGAAA	1320
Qy	1333	ATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1392
Db	1321	ATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTGAACCTATTGGT	1380
Qy	1393	GTTACTGGATCAAATCCAATAAGAAACTCCATGCTTAGAGTTGGAGTTGACTGGTC	1452
Db	1381	GTTACTGGATCAAATCCAATAAGAAACTCCATGCTTAGAGTTGGAGTTGACTGGTC	1440
Qy	1453	AGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGCTGTA	1512

Db	1441	AGCAGTGTGGTAAAGTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGCTGTA	1500
Qy	1513	TCCCGAGAACAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1572
Db	1501	TCCCGAGAACAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGACTAGCTAGAGAC	1560
Qy	1573	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACACGAAATCCTCTC	1632
Db	1561	AATGAATTAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACACGAGATCCTCTC	1620
Qy	1633	TCTGAAATCACTGAGCAGGAGAAAAGATTCTATGGAGTCACAGACACTATTGTGTAAC	1692
Db	1621	TCTGAAATCACTGAGCAGGAGAAAAGATTCTATGGAGTCACAGACACTATTGTGTAAC	1680
Qy	1693	ATCCCCGAAATTCTACCCAAATTGCTCTGTTAAATGGAATTCTAGAGATGAAGTA	1752
Db	1681	ATCCCCGAAATTCTACCCAAATTGCTCTGTTAAATGGAATTCTAGAGATGAAGTA	1740
Qy	1753	GCCCAGATGTATTGCTGGTAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1812
Db	1741	GCCCAGATGTATTGCTGGTAAAGATTGGCCTCCAATCAAACCTGAACAGGCTATGGAA	1800
Qy	1813	CTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTTGGTCTGGAA	1872
Db	1801	CTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTTGGTCTGGAA	1860
Qy	1873	AAATATTAAACAGATGACAAACTTTCTCAGTATTAAATTCACTGAGTACAGGTCTAAAA	1932
Db	1861	AAATATTAAACAGATGACAAACTTTCTCAGTATTAAATTCACTGAGTACAGGTCTAAAA	1920
Qy	1933	TATGAACAATATTGGATAACTGCTTGAGATTTTACTGAAGAAAGCATTGACTAAT	1992
Db	1921	TATGAACAATATTGGATAACTGCTTGAGATTTTACTGAAGAAAGCATTGACTAAT	1980
Qy	1993	CAAAGGATTGGGCACTTTCTTTGGCATTTAAATCTGAGATGCACAAATAAACAGTT	2052
Db	1981	CAAAGGATTGGGCACTTTCTTTGGCATTTAAATCTGAGATGCACAAATAAACAGTT	2040
Qy	2053	AGCCAGAGGTTGGCCTGCTTGGAGTCCTATTGCGTCATGGGATGTATTGAAG	2112
Db	2041	AGCCAGAGGTTGGCCTGCTTGGAGTCCTATTGCGTCATGGGATGTATTGAAG	2100
Qy	2113	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTATTAACCTTAACGTACATTCTAAA	2172
Db	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTATTAACCTTAACGTACATTCTAAA	2160
Qy	2173	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTTGAGCAAATGAGG	2232
Db	2161	CAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTTGAGCAAATGAGG	2220

Qy	2233	CGACCAGATTCATGGATGCCCTACAGGGCTGCTGTCCTCTAAACCTGCTCATCAA	2292
Db	2221	CGACCAGATTCATGGATGCCCTACAGGGCTGCTGTCCTCTAAACCTGCTCATCAA	2280
Qy	2293	CTAGGAAACCTCAGGCTAAAGAGTGTCAATTATGCTTCTGCAAAAGGCCACTGTGG	2352
Db	2281	CTAGGAAACCTCAGGCTAAAGAGTGTCAATTATGCTTCTGCAAAAGGCCACTGTGG	2340
Qy	2353	TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAAGAACATGAGATCATC	2412
Db	2341	TTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAAGAACATGAGATCATC	2400
Qy	2413	TTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATTATCGTATTATG	2472
Db	2401	TTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATTATCGTATTATG	2460
Qy	2473	GAAAATCTGGCAAAATCAAGGTCTGATCTTCAAGTGTACCTTATGGTTGCTGTCA	2532
Db	2461	GAAAATCTGGCAAAATCAAGGTCTGATCTTCAAGTGTACCTTATGGTTGCTGTCA	2520
Qy	2533	ATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACTATTATGCAAATT	2592
Db	2521	ATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACTATTATGCAAATT	2580
Qy	2593	CAGTGCAGGGCGCTGAAAGGTGCACTGCAGTTCAACAGGCCACACACTACATCAGTGG	2652
Db	2581	CAGTGCAGGGCGCTGAAAGGTGCACTGCAGTTCAACAGGCCACACACTACATCAGTGG	2640
Qy	2653	CTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTGTTACACGTTCA	2712
Db	2641	CTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTGTTACACGTTCA	2700
Qy	2713	TGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGTCACAATAGAAC	2772
Db	2701	TGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGTCACAATAGAAC	2760
Qy	2773	ATCATGGTAAAGACGATGGACAACGTTCATATAGATTGGACACTTTGGATCAC	2832
Db	2761	ATCATGGTAAAGACGATGGACAACGTTCATATAGATTGGACACTTTGGATCAC	2820
Qy	2833	AAGAAGAAAAATTGGTTAAACGAGAACGTGTGCCATTGTTTGACACAGGATTC	2892
Db	2821	AAGAAGAAAAATTGGTTAAACGAGAACGTGTGCCATTGTTTGACACAGGATTC	2880
Qy	2893	TTAATAGTAGTAAAGGAGCCAAGAACATGCACAAAGACAAGAGAATTGAGAGGTTT	2952
Db	2881	TTAATAGTAGTAAAGGAGCCAAGAACATGCACAAAGACAAGAGAATTGAGAGGTTT	2940

Qy 2953 CAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAATCTCTTCATAAAAT 3012  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 CAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAATCTCTTCATAAAAT 3000  
 Qy 3013 CTTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTGATGACATTGCA 3072  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 CTTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTGATGACATTGCA 3060  
 Qy 3073 TACATTGAAAGACCCTAGCCTAGATAAAAAGTAGAGCAAGAGGCTTGGAGTATTCATG 3132  
           ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 TACATTGAAAGACCCTAGCCTAGATAAAAAGTAGAGCAAGAGGCTTGGAGTATTCATG 3120  
 Qy 3133 AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTCCAC 3192  
           ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGATTGGATCTCCAC 3180  
 Qy 3193 ACAATTAAACAGCATGATTGAACTGAAAGATAACTGAGAAAATGAAAGCTACTCTGGA 3252  
           ||||||||||||||||||||||||||||||||||||||||  
 Db 3181 ACAATTAAACAGCATGATTGAACTGAAAGATAACTGAGAAAATGAAAGCTACTCTGGA 3240  
 Qy 3253 TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC 3312  
           ||||||||||||||||||||||||||||||||||||||||  
 Db 3241 TTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGGAATTGCAC 3300  
 Qy 3313 AATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACTATATAATTAAA 3372  
           ||||||||||||||||||||||||||||||||||||  
 Db 3301 AATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACTATATAATTAAA 3360  
 Qy 3373 TAATGTAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATTCAAAA 3424  
           ||||||||||||||||||||||||||||||||  
 Db 3361 TAATGTAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATTCAAAA 3412

## RESULT 10

ADU05935

ID ADU05935 standard; DNA; 3423 BP.

XX

AC ADU05935;

XX

DT 27-JAN-2005 (first entry)

XX

DE Novel bronchial cancer-associated human gene SeqID157.

XX

KW bronchial cancer; cytostatic; tumour-associated protein;

KW cancer detection; metastasis; tumour; gene; ds; human.

XX

OS Homo sapiens.

XX

PN DE10316701-A1.

PD 04-NOV-2004.  
XX  
PF 09-APR-2003; 2003DE-01016701.  
XX  
PR 09-APR-2003; 2003DE-01016701.  
XX  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
XX  
PI Mennerich D, Bruemmendorf T, Heiden E, Hermann K, Kinnemann H;  
PI Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;  
XX  
DR WPI; 2004-786403/78.  
DR P-PSDB; ADU06422.  
XX  
PT New nucleic acid, and derived proteins, useful for diagnosis of bronchial  
PT cancer and in screening for therapeutic and diagnostic agents.  
XX  
PS Claim 1; SEQ ID NO 157; 1381pp; German.  
XX  
CC This invention relates to a novel isolated nucleic acid associated with  
CC bronchial cancer comprising 489 defined sequences given in the  
CC specification. The invention may be useful for the production of  
CC compounds with a cytostatic activity through the inhibition of expression  
CC or activity of tumour-associated proteins. The novel DNA sequences and  
CC the proteins/peptides encoded by them are used for detecting bronchial  
CC cancer or determining the risk of developing it and to screen for  
CC specific binding partners of the DNA or protein sequences, where the  
CC binding partners are potentially useful as agents for treating or  
CC diagnosing bronchial cancer. The DNA or protein sequences can also be  
CC used for prognosis, detection of metastases and for secondary treatment  
CC (of tumours that have been stabilised or are no longer detectable).  
CC Detecting abnormal expression of the DNA sequences provides early  
CC diagnosis of bronchial cancers. The present sequence is that of a novel  
CC bronchial cancer-associated human gene sequence of the invention.  
XX  
SQ Sequence 3423 BP; 1134 A; 618 C; 709 G; 962 T; 0 U; 0 Other;  
  
Query Match 99.6%; Score 3410.4; DB 3; Length 3423;  
Best Local Similarity 99.9%;  
Matches 3422; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
  
Qy 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 60  
|||  
Db 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 60  
  
Ov 61 CCCCCAAGAACATCTAGTGGAAATGTTACTACCAAATGGAATGATAGTGAATTAGAATGC 120

Db	61	CCCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTAGAATGC	120
Qy	121	CTCCGTGAGGCTACATTAGTAACATAAAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCTACATTAGTAACATAAAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCGTAAGTGTACCCAGAA	240
Db	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCGTAAGTGTACCCAGAA	240
Qy	241	GCAGAAAGGGAGAATTTTGATGAAACAAGACGACTTGTGATCTCGGTTTCGAA	300
Db	241	GCAGAAAGGGAGAATTTTGATGAAACAAGACGACTTGTGATCTCGGTTTCGAA	300
Qy	301	CCATTTTAAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCATTTTAAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATGGTTTGCATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361	ATGGTTTGCATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTAGGGATCTT	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACCTCACAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACCTCACAGAG	540
Qy	541	CTGCCAAGCACATATATAATAATTGGATAGAGGCCAATAATGTTGATTGGTA	600
Db	541	CTGCCAAGCACATATATAATAATTGGATAGAGGCCAATAATGTTGATTGGTA	600
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACCTGCAAAATCAACCATGACTGTG	660
Db	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACCTGCAAAATCAACCATGACTGTG	660
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Qy	721	GAACAATTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAGTGTGGA	780
Db	721	GAACAATTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAGTGTGGA	780
Qy	781	TGTGATGAATACCTCCTAGAAAAATCCTCTGAGTCAGTATAAGTATAAGCTGT	840

Db	781	TGTGATGAATACTCCTAGAAAAATATCCTTGAGTCAGTATAAGTATAAGAAGCTGT	840
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	841	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	841	ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAAATAGAGCACTCAGAATA	1020
Db	961	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAAAATAGAGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Db	1021	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Db	1141	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGATCTT	1200
Qy	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTCTAAA	1260
Db	1201	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTCTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1261	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1381	AACCCTATTGGTGTACTGGATCAAATCCAAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTTGACTGGTTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1441	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1441	TTTGACTGGTTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGA	1560
Db	1501	.....   .....   .....   .....   .....   .....   .....   .....   .....	
Db	1501	AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCACGCAGGACTGAGTAACAGA	1560

Qy	1561	CTAGCTAGAGACAATGAATTAAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAGATTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAGATTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGGAACTTCTGGACTGTAAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGGAACTTCTGGACTGTAAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTTAATTCACTAGTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTTAATTCACTAGTAGTA	1920
Qy	1921	CAGGTCTAAATATGAACAATATTGGATAACTGCTGTGAGATTTACTGAAGAAA	1980
Db	1921	CAGGTCTAAATATGAACAATATTGGATAACTGCTGTGAGATTTACTGAAGAAA	1980
Qy	1981	GCATTGACTAATCAAAGGATTGGCACTTTTCTTTGGCATTTAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAATCAAAGGATTGGCACTTTTCTTTGGCATTTAAATCTGAGATGCAC	2040
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTGCATGGG	2100
Db	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTGCATGGG	2100
Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAAGCTCATTAACCTA	2160
Db	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAAGCTCATTAACCTA	2160
Qy	2161	GACATTCTAAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2161	GACATTCTAAACAGGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCACCAGATTCTATGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCACCAGATTCTATGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280

Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGTCAGGCTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGTCAGGCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Qy	2401	AATGAGATCATCTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2401	AATGAGATCATCTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Qy	2461	ATTCGTATTATGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGCAATCGGTGACTGTGTTGGACTTATTGAGGTGGTGCAGAACATTCTCACACT	2580
Db	2521	GGTTGTCTGCAATCGGTGACTGTGTTGGACTTATTGAGGTGGTGCAGAACATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCACTGCAAAGGCGGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGTCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATATGTCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTCATGTGCTGGACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701	TTTACACGTTCATGTGCTGGACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTGGACAC	2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTTATAACGAGAACGTGTGCCATTGTTTG	2880
Db	2821	TTTTGGATCACAAGAAGAAAAATTGGTTATAACGAGAACGTGTGCCATTGTTTG	2880
Qy	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTATCTAGCTATTGACAGCATGCCAAT	3000
Db	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTATCTAGCTATTGACAGCATGCCAAT	3000
Qy	3001	CTCTCATAAATCTTCTCAATGATGCTGGCTCTGGAACTACAAATCTTT	3060

Db	3001	CTCTTCATAAATCTTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTT	3060
Qy	3061	GATGACATTGCATACATCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3061	GATGACATTGCATACATCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Qy	3121	GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3121	GAGTATTTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Qy	3181	TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Db	3181	TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACTGAGAAAATGAAA	3240
Qy	3241	GCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCA	3300
Db	3241	GCTCACTCTGGATTCCACACTGCACTG-TAATAACTCTCAGCAGGCAAAGACCGATTGCA	3299
Qy	3301	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACT	3360
Db	3300	TAGGAATTGCACAATCCATGAACAGCATTAGATTACAGCAAGAACAGAAATAAAACT	3359
Qy	3361	ATATAATTAAATAATGAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTC	3420
Db	3360	ATATAATTAAATAATGAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCATTC	3419
Qy	3421	AAAA 3424	
Db	3420		
Db	3420	AAAA 3423	

## RESULT 11

ARC02473

ID ARC02473 standard; DNA; 3426 BP.

XX

AC ARC02473;

XX

DT 10-JUL-2008 (first entry)

XX

DE DNA fragments of a human Tox gene, 46524.

XX

KW DNA microarray; gene expression; drug screening; ds; Tox.

XX

OS Homo sapiens.

XX

PN US2007072175-A1.

XX

PD 29-MAR-2007.

XX  
PF 15-MAY-2006; 2006US-00433832.

XX  
PR 13-MAY-2005; 2005US-0680473P.  
PR 13-MAY-2005; 2005US-0680544P.

XX  
PA (BIOJ ) BIOGEN IDEC MA INC.

XX  
PI Cooper MT, Kinch D, Rosenberg M, Subramaniam SS, Szak ST, Li H;  
PI Bandaru R, Derbel M;

XX  
DR WPI; 2007-432796/41.

XX  
PT New nucleotide array comprises polynucleotide probes complementary to, or  
PT fragments of, Cynomolgus monkey genes, useful for detecting changes in  
PT gene expression upon administration of a therapeutic agent.

XX  
PS Claim 18; SEQ ID NO 46524; 33pp; English.

XX  
CC The new invention relates to a nucleotide array for detecting changes in  
CC gene expression upon administration of a therapeutic agent. The  
CC microarray has polynucleotide probes complementary to, or fragments of,  
CC Cynomolgus monkey genes, where each polynucleotide probe is immobilized  
CC to a discrete and known spot on a solid support. The polynucleotide  
CC probes are complementary to, or fragments of, any portion of an ortholog  
CC of a human gene, preferably a Tox gene. The probes are any of SEQ ID NO.  
CC 8882-9186. The probes are also complementary to, or fragments of, any  
CC portion of any of SEQ ID NO. 1-8881 or 9187-18598. The nucleotide array  
CC has at least one probe complementary to, or a fragment of, any portion of  
CC any human gene, where the probe from a human gene is any of SEQ ID NO.  
CC 43226-48714, or is complementary to, or a fragment of, any portion of any  
CC of SEQ ID NO. 43450-48714. The array has at least one probe complementary  
CC to, or a fragment of, any portion of any Rhesus monkey gene, where the  
CC probe from a Rhesus monkey gene is any of SEQ ID NO. 35841-36074, or is  
CC complementary to, or a fragment of, any portion of any of SEQ ID NO.  
CC 18599-35840 or 36075-43225. It also has at least one probe complementary  
CC to, or a fragment of, any portion of a Rhesus monkey gene and at least  
CC one probe complementary to, or a fragment of, any portion of any human  
CC gene. The nucleotide array is useful for detecting changes in gene  
CC expression upon administration of a therapeutic agent. It can be used for  
CC characterizing the actions, targets, and toxicities of therapeutic agents  
CC in primates, e.g. a human, a Cynomolgus monkey, or a Rhesus monkey. This  
CC sequence is a DNA fragment of a human Tox gene.

XX  
SQ Sequence 3426 BP; 1138 A; 623 C; 703 G; 962 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 6; Length 3426;  
Best Local Similarity 98.8%;  
Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACTGTGGGCATCCACTTGATG	60
Db	1	AGAATCAGAACATGCCTCCACGACCATCATCAGGTGAACTGTGGGCATCCACTTGATG	60
Qy	61	CCCCCAAGAACATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	61	CCCCCAAGAACATCCTAGTAGAATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Qy	121	CTCCGTGAGGCATCACATTAGTAACATAAACGATGAACATTAAAGAAGCAAGAAAATAC	180
Db	121	CTCCGTGAGGCATCACATTAAATAACCATAAACGATGAACATTAAAGAAGCAAGAAAATAC	180
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTACATTTCTGAAGTGTACCCAGAA	240
Db	181	CCCCTCCATCAACTTCTCAAGATGAATCTTACATTTCTGAAGTGTACTCAAGAA	240
Qy	241	GCAGAAAGGGAGAACATTTTGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Db	241	GCAGAAAGGGAGAACATTTTGATGAAACAAGACGACTTGTGACCTCGGTTTTCAA	300
Qy	301	CCATTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	301	CCCTTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Qy	361	ATTGGTTTGCATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	361	ATTGGTTTGCATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	421	CAGGACTTCCGAAGAAATATTCTGAACGTTGTAAGAAGCTGTGGATCTTAGGGACCTC	480
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGTCATCGCCACATGTAGAACATCTCACCAGAG	540
Db	481	AATTCACCTCATAGTAGAGCAATGTATGTCATCTCCAAATGTAGAACATCTCACCAGAA	540
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Db	541	TTGCCAAAGCACATATATAATAAAATTAGATAAGGCCAATAATAGTGGTGAATTGGTA	600
Qy	601	ATAGTTCTCCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCACCATGACTGTG	660
Db	601	ATAGTTCTCCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCACCATGACTGTG	660
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTCGAAGTATGTTGCTATCCTCT	720

Qy	721	GAACAAATTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Db	721	GAACAACTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTATATTTAAAAGTGTGGA	780
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAACGCT	840
Db	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAACGCT	840
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	841	ATAATGCTGGGAGGATGCCAATTGATGTTGATGGCTAAAGAAAGCCTTATTCTCAA	900
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAAATAGAGCACTCAGAATA	1020
Db	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGGTATAAATAGTGCACTCAGAATA	1020
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Db	1021	AAAATTCTTGCAACCTACGTGAATGTAATATCGAGACATTGATAAGATCTATGTT	1080
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGGCTGAATTATGATATACATTCCGTATCTT	1200
Db	1141	CCTTGTCCAATCCCAGGTGGAATGGCTGAATTATGATATACATTCCGTATCTT	1200
Qy	1201	CCTCGTGTGTCGACTTGGCTTCCATTGCTCTGTTAAAGGCGAAAGGGTGTAAA	1260
Db	1201	CCTCGTGTGTCGACTTGGCTTCCATTGCTCTGTTAAAGGCGAAAGGGTGTAAA	1260
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGGTGTGATTACACAGACACTCTA	1320
Db	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGGTGTGATTACACAGACACTCTA	1320
Qy	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1381	AACCCTATTGGTGTACTGGATCAAATCAAATAAAGAAACTCCATGCTTAGAGTTGGAG	1440
Qy	1441	TTGACTGGTTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500

Db	1441	TTTGACTGGTCAGCAGTGGTAAAGTCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Qy	1501	AATTGGCTGTATCCCAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGAACAGA	1560
Db	1501	AATTGGCTGTATCCCAGAAGCAGGATTAGCTATTCCCACGCAGGACTGAGAACAGA	1560
Qy	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTAAAGCAATTCTACA	1620
Db	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTAAAGCAATTCTACA	1620
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTCTATGGAGTCACAGACAC	1680
Db	1621	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAAGATTTCTATGGAGTCACAGACAC	1680
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAATTGCTCTGTCGTAAATGGAATTCT	1740
Db	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAATTGCTCTGTCGTAAATGGAATTCT	1740
Qy	1741	AGAGATGAACTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1741	AGAGATGAACTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1800
Qy	1801	CAGGCTATGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1801	CAGGCTATGAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Qy	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTAACTCAGCTAGTA	1920
Db	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTAACTCAGCTAGTA	1920
Qy	1921	CAGGTCTAAACATATGAACAAATTGGATAACTGCTGTGAGATTAACTGAAGAAA	1980
Db	1921	CAGGTCTAAACATATGAACAAATTGGATAACTGCTGTGAGATTAACTGAAGAAA	1980
Qy	1981	GCATTGACTAACAGGATGGGCACTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Db	1981	GCATTGACTAACAGGATGGGCACTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Qy	2041	AATAAACAGTTAGCCAGAGGTTGGCTGCTTGGAGTCCTATTGCGTCATGGGG	2100
Db	2041	AATAAACAGTTAGCCAGAGGTTGGCTGCTTGGAGTCCTATTGCGTCATGGGG	2100
Qy	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTA	2160
Db	2101	ATGTATTGAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTA	2160
Qy	2161	GACATTCTCAACAGGGAGAGGAAGGTGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220

Db	2161	GACATTCTCAACAGGAGAAGAAGGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Qy	2221	GAGCAAATGAGGCAGCCAGATTCATGGATGCCCTACAGGGCTTGTCTCCTCTAAAC	2280
Db	2221	GAGCAAATGAGGCAGCCAGATTCATGGATGCCCTACAGGGCTTGTCTCCTCTAAAC	2280
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Db	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Qy	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Db	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Qy	2461	ATTCGTATTATGAAAATATCTGCAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2461	ATTCGTATTATGAAAATATCTGCAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Qy	2521	GGTTGTCTGCAATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580
Db	2521	GGTTGTCTGCAATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGCTTGAAGGTGCACTGCAAGTCAACAGCCACACA	2640
Db	2581	ATTATGCAAATTCACTGCAAAGGCGGCTTGAAGGTGCACTGCAAGTCAACAGCCACACA	2640
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2701	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Db	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACGTGTTCATATAGATTTGGACAC	2820
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGTGCCATTGTTTG	2880
Db	2821	TTTTGGATCACAAGAAGAAAAATTGGTATAACGAGAACGTGTGCCATTGTTTG	2880
Qy	2881	ACACAGGATTCTTAATAGTGTAGTAAAGGAGCCAAAGAATGCACAAAGACAAGAGAA	2940
Db	2881	ACACAGGATTCTTAATAGTGTAGTAAAGGAGCCAAAGAATGCACAAAGACAAGAGAA	2940

Qy 2941 TTTGAGAGGTTTCAGGAGATGTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT 3000  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 TTTGAGAGGTTTCAGGAGATGTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT 3000

Qy 3001 CTCTTCATAAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTT 3060  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 CTCTTCATAAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTT 3060

Qy 3061 GATGACATTGCATACATCGAAAGACCCTAGCCTTAGATAAAAAGTGGACTGAGCAAGAGGCTTG 3120  
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 GATGACATTGCATACATCGAAAGACCCTAGCCTTAGATAAAAAGTGGACTGAGCAAGAGGCTTG 3120

Qy 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180  
           ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT 3180

Qy 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTG- AAAGATAACTGAGAAAATGAA 3239  
           ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAGAAAATGAA 3240

Qy 3240 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC 3299  
           ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC 3300

Qy 3300 ATAGGAATTGCACAATCCATGAACAGCATTAG- ATTACAGCAAGAACAGAAATAAAATA 3358  
           ||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 ATAGGAATTGCACAATCCATGAACAGCATTAGAATTACAGCAAGAACAGAAATAAAATA 3360

Qy 3359 CTATATAATTAAATAATGTAACAGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATT 3418  
           ||||||||||||||||||||||||||||||||||||||||  
 Db 3361 CTATATAATTAAATAATGTAACAGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATT 3420

Qy 3419 TCAAAA 3424  
           |||||||  
 Db 3421 TCAAAA 3426

## RESULT 12

AEK54940

ID AEK54940 standard; DNA; 3724 BP.

XX

AC AEK54940;

XX

DT 11-JUN-2007 (revised)

DT 16-NOV-2006 (first entry)

XX

DE Human PIK3CA DNA, SEQ ID NO:7.

XX

KW phosphoinositide-3-kinase, catalytic, alpha; PIK3CA; genetic marker;  
KW screening; adenocarcinoma; neoplasm; cytostatic; ds.

XX  
OS Homo sapiens.

XX  
PN WO2006094149-A2.

XX  
PD 08-SEP-2006.

XX  
PF 01-MAR-2006; 2006WO-US007493.

XX  
PR 01-MAR-2005; 2005US-0657841P.

XX  
PA (EXAC-) EXACT SCI CORP.

XX  
PI Shuber AP;

XX  
DR WPI; 2006-680485/70.

DR REFSEQ; NM\_006218.

DR PC:NCBI; gi54792081.

DR PC\_ENCPRO:NCBI; gi54792082.

XX  
PT Screening for adenoma in a subject, comprises testing a sample for the  
PT presence of each of a panel of genetic markers, where the panel is more  
PT than 60% informative for adenoma.

XX  
PS Disclosure; SEQ ID NO 7; 79pp; English.  
XX

CC The invention relates to a method for screening a subject for the  
CC presence of adenoma. The method comprises interrogating a sample from the  
CC subject for each of a panel of genetic markers, where the panel is more  
CC than 60% informative for adenoma, and where the presence of one or more  
CC of the markers is indicative of adenoma. Also described are: (1) a method  
CC of detecting indicia of adenoma, by assaying a sample from a subject for  
CC the presence of one or more genetic abnormalities from a group of genetic  
CC abnormalities that is more than 60% informative for adenoma; (2) a method  
CC of detecting adenoma in a subject, by performing an assay on a sample  
CC from the subject that is more than 60% informative for adenoma; and (3) a  
CC kit comprising a group of oligonucleotides, where each oligonucleotide is  
CC adapted for interrogating a genetic locus for the presence of a marker  
CC from a panel that is at least 60% informative for adenoma. The methods  
CC and kit of the invention are useful for screening for adenoma in a  
CC subject. The adenoma is especially a colonic and/or invasive adenoma. The  
CC methods can detect adenoma at an early stage with a high level of  
CC confidence, increasing the chances of successful treatment. This sequence  
CC represents a human DNA sequence that can be used as a genetic marker in  
CC the method of the invention.

CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed

CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 4; Length 3724;  
 Best Local Similarity 98.8%;  
 Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACATGCCTCCACGACCATCATCAGGTGAACGTGGGCATCCACTTGATG	205
Qy	61	CCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTAAAGATGC	120
Db	206	CCCCAAGAACCTAGTGAATGTTACTACCAAATGGAATGATAGTGACTTAAAGATGC	265
Qy	121	CTCGTGAGGCTACATTAGTAACATAAGCATGAACATTAAAGCAAGAAAATAC	180
Db	266	CTCGTGAGGCTACATTAAATAACCATAAGCATGAACATTAAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCCAGAA	240
Db	326	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACTCAAGAA	385
Qy	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Db	386	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGACCTCGGTTTTCAA	445
Qy	301	CCATTTTAAAGTAATTGAAACAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCATTTTAAAGTAATTGAAACAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCAATTGATATGGTAAAGATCCTGAAGTA	420
Db	506	ATGGTTTGCTATCGGCATGCCAGTGTGCAATTGATATGGTAAAGATCCTGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATTCTTAATGTTGAAAGAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATTCTGAACGTTGAAAGAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTACACCTCATAGTAGAGCAATGTATGCTATCCGCCACATGTAGAAATCTCACAGAG	540
Db	626	AATTACACCTCATAGTAGAGCAATGTATGCTATCCCAAATGTAGAAATCTCACAGAA	685
Qy	541	CTGCCAAAGCACATATAATAAAATTGGATAGAGGCAAAATAAGTGGTGTATGGGTA	600
Db	686	TTGCCAAAGCACATATAATAAAATTAGATAAAGGGCAAAATAAGTGGTGTATGGGTA	745
Qy	601	ATAGTTCTCCAAATAATGACAAGCAGAAAGTATACTCTGAAAATCAACCATGACTGTG	660

Db	746	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGA	805
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTCGAAGTATGTTGCTATCCCTCT	865
Qy	721	GAACAAATTAAACTCTGTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Db	866	GAACAACTAAACTCTGTTAGAATATCAGGGCAAGTATTTAAAAGTGTGGA	925
Qy	781	TGTGATGAAACTTCCTAGAAAATATCCTCTGAGTCAGTATAAGTATAAGAAGCTGT	840
Db	926	TGTGATGAAACTTCCTAGAAAATATCCTCTGAGTCAGTATAAGTATAAGAAGCTGT	985
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	986	ATAATGCTGGGAGGATGCCAATTGATGTTGATGGCTAAAGAAAGCCTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGTGCACTCAGAATA	1165
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1166	AAAATTCTTGCAACCTACGTGAATGTAATATTGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCAGGAGAACCTTATGTGACAATGTGAACACTCAAAGAGTA	1285
Qy	1141	CCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCGTACCTT	1200
Db	1286	CCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCCGTACCTT	1345
Qy	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1346	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAAACTTGTGATTACACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGAAATATAAAACTTGTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380

Db	1466	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1525
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAAACCTCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAAACCTCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1765
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAAGATTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAAGATTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAAATTACCCAGATCTATGGTCGAGGTTTGCTGTT	1860
Db	1946	CAGGCTATGGAACCTCTGGACTGTAAATTACCCAGATCTATGGTCGAGGTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTAAATTACAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATATTAACAGATGACAAACTTCTCAGTATTAAATTACAGCTAGTA	2065
Qy	1921	CAGGTCTAAATATGAACAAATTTGGATAACTTGCTGTGAGATTAACTGAAGAAA	1980
Db	2066	CAGGTCTAAATATGAACAAATTTGGATAACTTGCTGTGAGATTAACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATGGGACTTTTCTTTGGCATTAAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATGGGACTTTTCTTTGGCATTAAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCTGCTTGGAGTCCTATTGCGTGCATGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTGGCTGCTTGGAGTCCTATTGCGTGCATGGG	2245

Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAAC	2160
Db	2246	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAAC	2305
Qy	2161	GACATTCTCAAACAGGGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCAGCCAGATTCATGGATGCCCTACAGGGCTTGTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCAGCCAGATTCATGGATGCCCTACAGGGCTTGTCTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGAAATTATGCTTCCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGAAATTATGCTTCCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2545
Qy	2401	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGAAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGAAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAACCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTGGACTTATTGAGGTGGTGCAGAACCTCACACT	2725
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCACTGCAAAGGCGGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2846	TTTACACGTTCATGTGCTGGATACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACTGTTCATATAGATTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTAAAGACGATGGACAACTGTTCATATAGATTGGACAC	2965

Qy	2821	TTTTGGATACAAGAAGAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTTTG	2880
Db	2966	TTTTGGATACAAGAAGAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTTTG	3025
Qy	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGTTATCTAGCTATTGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGTTATCTAGCTATTGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAATCTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTT	3060
Db	3146	CTCTTCATAAATCTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACAATCTTT	3205
Qy	3061	GATGACATTGCATACATTGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3206	GATGACATTGCATACATTGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3265
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3326	TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTAAATAATGTAACAGCAAACAGGGTTGATAGCACTTAAACTAGTCATT	3418
Db	3506	CTATATAATTAAATAATGTAACAGCAAACAGGGTTGATAGCACTTAAACTAGTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

RESULT 13

AER29796

ID AER29796 standard; DNA; 3724 BP.

XX

AC AER29796;  
XX  
DT 11-JUN-2007 (revised)  
DT 22-MAR-2007 (first entry)  
XX  
DE Breast cancer-associated gene SEQ ID NO:97.  
XX  
KW diagnosis; breast tumor; biochip; tumor marker; genetic marker;  
KW biomarker; DNA detection; RNA detection; ds; PIK3CA.  
XX  
OS Homo sapiens.  
XX  
PN WO2007006911-A2.  
XX  
PD 18-JAN-2007.  
XX  
PF 05-JUL-2006; 2006WO-FR001593.  
XX  
PR 07-JUL-2005; 2005FR-00052087.  
XX  
PA (INMR ) BIOMERIEUX SA.  
XX  
PI Krause A, Leissner P, Mougin B, Paye M;  
XX  
DR WPI; 2007-138577/14.  
DR PC:NCBI; gi54792081.  
DR PC\_ENCPRO:NCBI; gi54792082.  
XX  
PT In vitro diagnosis of breast cancer comprises extracting biological  
PT material of biological sample, contacting biological material with  
PT specific reagents of target genes and determining target gene expression.  
XX  
PS Example 2; SEQ ID NO 97; 305pp; French.  
XX  
CC The invention describes a method for in vitro diagnosis of breast cancer  
CC in a patient susceptible to be affected by breast cancer, comprising:  
CC extracting nucleic acid from a biological sample taken from the patient;  
CC contacting the nucleic acid with at least 8 hybridization probes for  
CC detection of target genes chosen from SEQ ID Nos. 1 to 8 or 10 probes for  
CC detection of target genes chosen from SEQ ID Nos. 1, 2, 4, 6, 13, 14, 26,  
CC 69, 81 and 105; and determining the expression of the target genes. The  
CC invention also includes: a support, such as a biochip, comprising at  
CC least 8 or 10 hybridization probes mentioned above; and a diagnosis kit  
CC for breast cancer comprising the support. The method, biochip and kit are  
CC useful for the in vitro diagnosis of breast cancer. This sequence is a  
CC breast cancer-associated gene.  
CC  
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed  
CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 5; Length 3724;  
 Best Local Similarity 98.8%;  
 Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACATGCCTCCACGACCATCATCAGGTGAACGTGGGCATCCACTTGATG	205
Qy	61	CCCCCAAGAACATCTAGTGGATGTTACTACCAAATGGAATGATAGTGTACTTAAAGAATGC	120
Db	206	CCCCCAAGAACATCTAGTGGATGTTACTACCAAATGGAATGATAGTGTACTTAAAGAATGC	265
Qy	121	CTCCGTGAGGCTACATTAGTAACATAAGCATGAACATTAAAGAAGCAAGAAAATAC	180
Db	266	CTCCGTGAGGCTACATTAATAACCATAAAAGCATGAACATTAAAGAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCTTACAGAA	240
Db	326	CCCCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGAAGTGTACCTAAGAA	385
Qy	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGCTTTCAA	300
Db	386	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGACCTCGGCTTTCAA	445
Qy	301	CCATTAAAGTAATTGAAACAGTAGGCCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCATTAAAGTAATTGAAACAGTAGGCCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATTGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	506	ATTGGTTTGCTATCGGCATGCCAGTGTGAAATTGATATGGTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTCCGAAGAAATATTCTGAACGTTGTAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTACACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAATCTCACCAAGAG	540
Db	626	AATTACACCTCATAGTAGAGCAATGTATGCTATCCTCAAATGTAGAATCTCACCAAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAAATAATGGTGATTGGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAAATTAGATAAAGGCCAAATAATGGTGATTGGGTA	745
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTG	660

Db	746	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTA	805
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAGTAATTGCTGAAGCAATCAGGGAAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAAATTAAAACCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Db	866	GAACAACTAAAACCTGTGTTTAGAATATCAGGGCAAGTATATTTAAAAGTGTGGA	925
Qy	781	TGTGATGAACTACTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATAAGAAGCTGT	840
Db	926	TGTGATGAACTACTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATAAGAAGCTGT	985
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	986	ATAATGCTGGGAGGATGCCAATTGATGTTGATGCCAAAGAAAGCCTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAAACATCTACAAAATCCCTTGGTTATAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAAACATCTACAAAATCCCTTGGTTATAATAGTCAGACTCAGAATA	1165
Qy	1021	AAAATTCTTGTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1166	AAAATTCTTGTGCAACCTACGTGAATGTAATATTGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGTACTT	1200
Db	1286	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATTCTGTACTT	1345
Qy	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1346	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGGAAATAAAACTTGTGATTACACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGGAAATAAAACTTGTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1466	GTATCTGGAAAAATGGCTTGAATCTTGGCCAGTACCTCATGGATTAGAAGATTGCTG	1525

Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAAACCTCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCTATTGGTGTACTGGATCAAATCCAATAAAGAAAACCTCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGACTGGTTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGACTGGTTCAGCAGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAACAGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAAGGGAAAATGACAAAGAACAGCTCAAAGCAATTCTACA	1765
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAGATTGGCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1946	CAGGCTATGGAACTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATATTAACAGATGACAAACATTCTCAGTATTAAATTCTAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATATTAACAGATGACAAACATTCTCAGTATTAAATTCTAGCTAGTA	2065
Qy	1921	CAGGTCTAAATATGAACAAATTGGATAACTTGCTTGTGAGATTAACTGAAGAAA	1980
Db	2066	CAGGTCTAAATATGAACAAATTGGATAACTTGCTTGTGAGATTAACTGAAGAAA	2125
Qy	1981	GCATTGACTAACAGGATTGGGACTTTCTTTGGCATTAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAACAGGATTGGGACTTTCTTTGGCATTAAATCTGAGATGCAC	2185
Qy	2041	AATAAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTGCATGTGGG	2100
Db	2186	AATAAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTGCATGTGGG	2245

Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGCATGGAAAAGCTCATTAACCTAAC	2160
Db	2246	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGCATGGAAAAGCTCATTAACCTAAC	2305
Qy	2161	GACATTCTCAAACAGGGAGAGGAAGGTGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGGAGAAGAAGGTGAAACACAAAAGGTACAGATGAAGTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCACCAGATTCATGGATGCCCTACAGGGCTTGCTCTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCACCAGATTCATGGATGCTCACAGGGCTTCTGCTCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGCTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2545
Qy	2401	AATGAGATCATTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGAAAATATCTGGAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGAAAATATCTGGAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGGACTTATTGAGGTGGTGCAGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCACTGCAAAGGCGGCTTGAAGGTGCACTGCAGTTCAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2846	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAACTGTTCATATAGATTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTAAAGACGATGGACAACTGTTCATATAGATTGGACAC	2965
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTTATAACGAGAACGTGTGCCATTGTTTG	2880

Db	2966	TTTTGGATCACAGAAGAAAAATTGGTTATAACGAGAACGTGTGCCATTGTTTG	3025
Qy	2881	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGCCAAAGAACATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTCTTAATAGTGATTAGTAAAGGAGCCAAAGAACATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACACAGATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACACAGATGCCAAT	3145
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTTGGAAATGCCAGAACTACAATCTTT	3060
Db	3146	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTTGGAAATGCCAGAACTACAATCTTT	3205
Qy	3061	GATGACATTGCATACATTGAAAGACCCTAGCCTTAGATAAAAAGACTGAGCAAGAGGCTTG	3120
Db	3206	GATGACATTGCATACATTGAAAGACCCTAGCCTTAGATAAAAAGACTGAGCAAGAGGCTTG	3265
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3326	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTAAATAATGAAACGCAAACAGGGTTGATGCACTTAAACTAGTTCATT	3418
Db	3506	CTATATAATTAAATAATGAAACGCAAACAGGGTTGATGCACTTAAACTAGTTCATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

### RESULT 14

ARV60468

ID ARV60468 standard; cDNA; 3724 BP

xx

AC ARV60468

XX  
DT 24-JUL-2008 (first entry)  
XX  
DE Human PIK3CA polynucleotide, SEQ ID 30.  
XX  
KW mutation; dna microarray; prognosis; diagnostic test; therapeutic;  
KW non-small-cell lung cancer; tumor; cytostatic; ss; gene;  
KW phosphoinositide-3-kinase, catalytic, alpha polypeptide; PIK3CA.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 158. .3364  
FT /\*tag= a  
FT /product  
XX  
PN WO2008061213-A2.  
XX  
PD 22-MAY-2008.  
XX  
PF 15-NOV-2007; 2007WO-US084888.  
XX  
PR 16-NOV-2006; 2006US-0866103P.  
PR 10-JUL-2007; 2007US-0948818P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Seshagiri S, Peters B, Kan Z;  
XX  
DR WPI; 2008-G25985/39.  
DR P-PSDB; ARV60505.  
DR PC:NCBI; gi54792081.  
DR PC\_ENCPRO:NCBI; gi54792082.  
XX  
PT New isolated polynucleotide comprises PRO polynucleotide or fragment  
PT comprising a nucleotide variation, useful for detecting nucleotide  
PT variations for diagnosing and treating tumors.  
XX  
PS Claim 2; SEQ ID NO 30; 55pp; English.  
XX  
CC The present invention relates to a novel isolated polynucleotide  
CC comprising a PRO polynucleotide or its fragment. The PRO polynucleotide  
CC or its fragment comprises a nucleotide variation at a nucleotide position  
CC given in the specification. A nucleotide variation refers to a change in  
CC a nucleotide sequence (e.g., an insertion, deletion, inversion, or  
CC substitution of one or more nucleotides, such as a single nucleotide  
CC polymorphism (SNP)) relative to a reference sequence (e.g., a wild type  
CC sequence). A nucleotide variation may be a somatic mutation or a germline  
CC polymorphism. The present invention provides: (i) an allele-specific

CC oligonucleotide that hybridizes to a region of a PRO polynucleotide  
 CC comprising a nucleotide variation at a nucleotide position, or its  
 CC complement; (ii) a kit comprising the oligonucleotide and an enzyme;  
 CC (iii) a microarray comprising the oligonucleotide; (iv) a method for  
 detecting the absence or presence of the variation at a nucleotide  
 CC position; (v) a method for amplifying a nucleic acid comprising the  
 CC nucleotide variation; (vi) a method for determining the genotype of a  
 CC biological sample (e.g. non-small cell lung carcinoma sample) from a  
 CC mammal; (vii) a method for classifying a tumor in the mammal; and (viii)  
 CC a method for predicting whether a tumor (e.g. non-small cell lung  
 CC carcinoma) will respond to a therapeutic agent that targets a PRO or a  
 CC PRO polynucleotide, comprises determining whether the tumor comprises a  
 CC variation in a PRO or PRO polynucleotide, where the presence of a  
 CC variation indicates that the tumor will respond to the therapeutic agent.  
 CC The method of detecting the absence or presence of the nucleotide  
 CC variation comprises: (a) contacting the suspected nucleic acid with the  
 CC allele-specific oligonucleotide that is specific for the nucleotide  
 CC variation, under conditions suitable for hybridization of the  
 CC oligonucleotide to the nucleic acid; and (b) detecting the absence or  
 CC presence of allele-specific hybridization. The method of amplifying the  
 CC nucleic acid comprising the nucleotide variation comprises: (a)  
 CC contacting the nucleic acid with a primer that hybridizes to the nucleic  
 CC acid at 3' of the nucleotide variation; and (b) extending the primer to  
 CC generate an amplification product comprising the nucleotide variation.  
 CC The isolated polynucleotide is used for detecting nucleotide variations.  
 CC The methods are used for diagnosing and treating tumors. The present  
 CC sequence is a human PRO polynucleotide sequence used in the invention.  
 CC

CC Revised record issued on 18-JUN-2008 : Enhanced with precomputed  
 CC information from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 7; Length 3724;  
 Best Local Similarity 98.8%;  
 Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy 1 AGGATCAGAACAAATGCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 60  
 |||||||

Db 146 AGAACATCAGAACAAATGCCTCCACGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 205

Qy 61 CCCCAAGAACATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTGAATGC 120  
 |||||||

Db 206 CCCCAAGAACATCCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTGAATGC 265

Qy 121 CTCCGTGAGGCTACATTAGTAACATAAACGATGAACATTAAAGAAGCAAGAAAATAC 180  
 |||||||

Db 266 CTCCGTGAGGCTACATTAAATAACCATAAACGATGAACATTAAAGAAGCAAGAAAATAC 325

Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGTAAGTGTACCCAAGAA	240
Db	326	CCCCTCCATCAACTTCTCAAGATGAATCTTCTACATTTCTGTAAGTGTACTCAAGAA	385
Qy	241	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGATCTCGGCTTTCAA	300
Db	386	GCAGAAAGGGAGAATTGGATGAAACAAGACGACTTGTGACCTCGGCTTTCAA	445
Qy	301	CCATTTAAAAGTAATTGAAACAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTAAAAGTAATTGAAACAGTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATATGGTAAAGATCCTGAAGTA	420
Db	506	ATGGTTTGCTATCGGCATGCCAGTGTGGAATTGATATGGTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCAGAAGAAATTCTTAATGTTGTAAGAACGCTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCAGAAGAAATTCTGAACGTTGTAAGAACGCTGGATCTTAGGGACCTC	625
Qy	481	AATTCACCTCATAGTAGAGCAATGTATGCTATCGCCACATGTAGAACATCTCACCAGAG	540
Db	626	AATTCACCTCATAGTAGAGCAATGTATGCTATCCTCAAATGTAGAACATCTCACCAGAA	685
Qy	541	CTGCCAAAGCACATATATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Db	686	TTGCCAAAGCACATATATAAAATTAGATAAGGCCAATAATAGTGGTGAATTGGTA	745
Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	746	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	805
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAAACTCGAAGTATGTTGCTATCCTCT	865
Qy	721	GAACAATTAAAACTCTGTGTTTAGAATATCAGGGCAAGTACATTTAAAAGTGTGGA	780
Db	866	GAACAACAAAATCTGTGTTTAGAATATCAGGGCAAGTATTTAAAAGTGTGGA	925
Qy	781	TGTGATGAATACCTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	840
Db	926	TGTGATGAATACCTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGT	985
Qy	841	ATAATGCTGGGAGGATGCCAATTGAGATGATGGCTAAAGAACGCTTTATTCTCAA	900
Db	986	ATAATGCTGGGAGGATGCCAATTGATGGCTAAAGAACGCTTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCA	960

Db	1046	CTGCCAATGGACTGTTTACAATGCCATTTCAGACGCATTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGTCACTCAGAATA	1165
Qy	1021	AAATTCTTGCAACCTACGTGAATCTAAATATCGAGACATTGACAAGATTATGTT	1080
Db	1166	AAATTCTTGCAACCTACGTGAATGTAATATCGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCATGGAGGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1285
Qy	1141	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1286	CCTTGTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1345
Qy	1201	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTAAA	1260
Db	1346	CCTCGTGTGTCGACTTGCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGTAAA	1405
Qy	1261	GAGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1406	GAGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380
Db	1466	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1525
Qy	1381	AACCCTATTGGTGTACTGGATCAAATCCAATAAGAAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCCTATTGGTGTACTGGATCAAATCCAATAAGAAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTGACTGGTCAGCAGTGTGTTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTGACTGGTCAGCAGTGTGTTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGCTGTATCCCGAGAACAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGCTGTATCCCGAGAACAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAATGACAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAATGACAAGAACAGCTCAAAGCAATTCTACA	1765
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680

Db	1766	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGCTGTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGCTGTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCCAGATGTATTGCTGGTAAAAGATTGCCCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCCAGATGTATTGCTGGTAAAAGATTGCCCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCATGGTCGAGGTTTGCTGTT	1860
Db	1946	CAGGCTATGGAACCTCTGGACTGTAATTACCCAGATCCATGGTCGAGGTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTTAACAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTTAACAGCTAGTA	2065
Qy	1921	CAGGTCTAAATATGAAACATATTGGATAACTGCTGTGAGATTAACTGAAGAAA	1980
Db	2066	CAGGTCTAAATATGAAACATATTGGATAACTGCTGTGAGATTAACTGAAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGCACTTTCTTTGGCATTTAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGCACTTTCTTTGGCATTTAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTGTGGG	2100
Db	2186	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTTGGAGTCCTATTGCGTGTGGG	2245
Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAGCTCATTAACTTA	2160
Db	2246	ATGTATTGAAAGCACCTGAATAGGCAAGTCGAGGAATGGAAAGCTCATTAACTTA	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAGGTACAGATGAAGTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAGGTACAGATGAAGTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCACCAGATTCTATGGATGCCCTACAGGGCTTGCTCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCACCAGATTCTATGGATGCTCACAGGGCTTCTGCTCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTAAAGAGTGTGCAATTATGCTCTGCAAAA	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTGAGAGTGTGCAATTATGCTCTGCAAAA	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2400
Db	2486	AGGCCACTGTGGTTGAATTGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAGAAC	2545

Qy	2401	AATGAGATCATCTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2460
Db	2546	AATGAGATCATCTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT	2605
Qy	2461	ATTCGTATTATGGAAAATATCTGGAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGGAAAATATCTGGAAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCTGTCAATCGGTGACTGTGTTGGACTTATTGAGGTGGTGGCGAAATTCTCACACT	2580
Db	2666	GGTTGTCTGTCAATCGGTGACTGTGTTGGACTTATTGAGGTGGTGGCGAAATTCTCACACT	2725
Qy	2581	ATTATGCAAATTCAAGTGCAAAGGC GGCTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCAAGTGCAAAGGC GGCTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2785
Qy	2641	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAAATATATGATGCA GCCATTGACCTG	2700
Db	2786	CTACATCAGTGGCTCAAAGACAAGAACAAAGGAGAAAATATATGATGCA GCCATTGACCTG	2845
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2846	TTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTGAAGACGATGGACAACTGTTCATATAGATTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTGAAGACGATGGACAACTGTTCATATAGATTGGACAC	2965
Qy	2821	TTTTGGATCACAAGAAGAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTTTG	2880
Db	2966	TTTTGGATCACAAGAAGAAAAATTGGTTATAAACGAGAACGTGTGCCATTGTTTG	3025
Qy	2881	ACACAGGATTCTTAATAGT GATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTCTTAATAGT GATTAGTAAAGGAGGCCAAGAACATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATCGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATCGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAAATCTTT	3060
Db	3146	CTCTTCATAAAATCTTCTCAATGATGCTGGCTCTGGAAATGCCAGAACTACAAATCTTT	3205
Qy	3061	GATGACATTGCATACATTGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3206	GATGACATTGCATACATTGAAAGACCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3265

Qy	3121 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266 GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181 TGGATCTCCACACAATTAAACAGCATGCATTGAAGT-G-AAGATAACTGAGAAAATGAA	3239
Db	3326 TGGATCTCCACACAATTAAACAGCATGCATTGAAGT-G-AAGATAACTGAGAAAATGAA	3385
Qy	3240 AGCTCACTCTGGATTCCACACTGCAGTGTAAATAACTCTCAGCAGGCAAAGACCATTGC	3299
Db	3386 AGCTCACTCTGGATTCCACACTGCAGTGTAAATAACTCTCAGCAGGCAAAGACCATTGC	3445
Qy	3300 ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTACAGCAAGAACAGAAATAAAATA	3358
Db	3446 ATAGGAATTGCACAATCCATGAACAGCATTAGAATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359 CTATATAATTAAATAATGTAACCGCAAACAGGGTTGATAGCACTTAAACTAGTCATT	3418
Db	3506 CTATATAATTAAATAATGTAACCGCAAACAGGGTTGATAGCACTTAAACTAGTCATT	3565
Qy	3419 TCAAAA 3424	
Db	3566 TCAAAA 3571	

## RESULT 15

ARW65283

ID ARW65283 standard; cDNA; 3724 BP.

XX

AC ARW65283;

XX

DT 07-AUG-2008 (first entry)

XX

DE Human PIK3CA cDNA, SEQ ID 53.

XX

KW tumor marker; prognosis; diagnostic test; cancer; ss; gene; PIK3CA.

XX

OS Homo sapiens.

XX

PN WO2008070325-A2.

XX

PD 12-JUN-2008.

XX

PF 24-OCT-2007; 2007WO-US082397.

XX

PR 26-OCT-2006; 2006US-0863106P.

PR 14-MAY-2007; 2007US-0917814P.

XX

PA (GETH ) GENENTECH INC.

XX  
PI Kan Z, Kenski DM, Peters B, Seshagiri S;  
XX

DR WPI; 2008-G69314/42.

DR P-PSDB; ARW65361.

DR PC:NCBI; gi54792081.

DR PC\_ENCPRO:NCBI; gi54792082.

XX

PT New polynucleotide, useful for determining the genotype of a sample from  
PT a mammal, for classifying a tumor in a mammal or for predicting whether a  
PT tumor will respond to a therapeutic agent that targets a PRO polypeptide  
PT or polynucleotide.

XX

PS Claim 2; SEQ ID NO 53; 98pp; English.

XX

CC The present invention relates to novel isolated polynucleotides. An  
CC isolated polynucleotide comprises: (a) a PRO polynucleotide or its  
CC fragment that is at least about 10 nucleotides in length or that  
CC comprises a nucleotide variation at a nucleotide position given in the  
CC specification, or (b) its complement. These variations provide biomarkers  
CC for cancer and/or predisposition to tumorigenesis or tumor promotion. The  
CC present invention provides: (1) a kit comprising the oligonucleotide and  
CC at least one enzyme; (2) a microarray comprising the oligonucleotide; (3)  
CC a method for detecting the absence or presence of a nucleotide variation  
CC at a nucleotide position given in the specification, which comprises  
CC contacting the nucleic acid suspected of comprising the nucleotide  
CC variation with an allele-specific oligonucleotide that is specific for  
CC the nucleotide variation and detecting the absence or presence of allele-  
CC specific hybridization; (4) a method for amplifying a nucleic acid  
CC comprising a nucleotide variation at a nucleotide position given in the  
CC specification; (5) a method for determining the genotype of a tumor  
CC sample from a mammal; (6) a method for classifying a tumor in a mammal by  
CC detecting the presence of a variation in a PRO or PRO polynucleotide in a  
CC biological sample derived from the mammal; and (7) a method for  
CC predicting whether a tumor will respond to a therapeutic agent that  
CC targets a PRO or a PRO polynucleotide by determining whether the tumor  
CC comprises a variation in a PRO or PRO polynucleotide, where the presence  
CC of a variation indicates that the tumor will respond to the therapeutic  
CC agent. The method of amplifying a nucleic acid comprising a nucleotide  
CC variation comprises: (a) contacting the nucleic acid with a primer that  
CC hybridizes to the nucleic acid at a sequence 3' of the nucleotide  
CC variation, and (b) extending the primer to generate an amplification  
CC product comprising the nucleotide variation. The variations disclosed in  
CC the invention are useful in methods and compositions related to cancer  
CC diagnosis and therapy. The present sequence is an isolated polynucleotide  
CC of the invention.

CC

CC Revised record issued on 09-JUL-2008 : Enhanced with precomputed infor

CC

CC

CC Revised record issued on 09-JUL-2008 : mation from BOND.

XX

SQ Sequence 3724 BP; 1242 A; 684 C; 763 G; 1035 T; 0 U; 0 Other;

Query Match 97.5%; Score 3338; DB 7; Length 3724;  
 Best Local Similarity 98.8%;  
 Matches 3384; Conservative 0; Mismatches 40; Indels 2; Gaps 2;

Qy	1	AGGATCAGAACATGCCTCCAAGACCATCATCAGGTGAACGTGGGCATCCACTTGATG	60
Db	146	AGAATCAGAACATGCCTCCACGACCATCATCAGGTGAACGTGGGCATCCACTTGATG	205
Qy	61	CCCCCAAGAACCTAGTGGATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	120
Db	206	CCCCCAAGAACCTAGTAGAATGTTACTACCAAATGGAATGATAGTGACTTTAGAATGC	265
Qy	121	CTCGTGAAGCTACATTAGTAACATAAACGATGAACATTAAAGCAAGAAAATAC	180
Db	266	CTCGTGAAGCTACATTAAATAAACATAAACGATGAACATTAAAGCAAGAAAATAC	325
Qy	181	CCTCTCCATCAACTTCTCAAGATGAATCTTACATTTCTGAAGTGTTACCCAGAA	240
Db	326	CCCCTCCATCAACTTCTCAAGATGAATCTTACATTTCTGAAGTGTTACTCAAGAA	385
Qy	241	GCAGAAAGGGAGAACATTGGATGAAACAAGACGACTTGTGATCTCGGTTTTCAA	300
Db	386	GCAGAAAGGGAGAACATTGGATGAAACAAGACGACTTGTGACCTCGGTTTTCAA	445
Qy	301	CCATTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	360
Db	446	CCCTTTAAAGTAATTGAACCACTAGGCAACCGTGAAGAAAAGATCCTCAATCGAGAA	505
Qy	361	ATGGTTTGCTATCGGCATGCCAGTGTGCGAATTGATGGTAAAGATCCTGAAGTA	420
Db	506	ATGGTTTGCTATCGGCATGCCAGTGTGGAATTGATGGTAAAGATCCAGAAGTA	565
Qy	421	CAGGACTTCCGAAGAAATATTCTTAATGTTGTAAGAAGCTGTGGATCTTAGGGATCTT	480
Db	566	CAGGACTTCCGAAGAAATATTCTGAACGTTGTAAGAAGCTGTGGATCTTAGGGACCTC	625
Qy	481	AATTACACCTCATAGTAGAGCAATGTATGTCTATCGCCACATGTAGAACATTCTCACAGAG	540
Db	626	AATTACACCTCATAGTAGAGCAATGTATGTCTATCCTCAAATGTAGAACATTCTCACAGAA	685
Qy	541	CTGCCAAAGCACATATATAATAAAATTGGATAGAGGCCAATAATAGTGGTGAATTGGTA	600
Db	686	TTGCCAAAGCACATATATAATAAAATTAGATAAAGGCCAATAATAGTGGTGAATTGGTA	745

Qy	601	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	660
Db	746	ATAGTTCTCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTG	805
Qy	661	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGCTATCATCT	720
Db	806	CCAGAACAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATCCCTCT	865
Qy	721	GAACAACTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTACATTAAAAGTGTGTGGA	780
Db	866	GAACAACTAAAACCTCTGTGTTTAGAATATCAGGGCAAGTATATTAAAAGTGTGTGGA	925
Qy	781	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATAAGAAGCTGT	840
Db	926	TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATAAGAAGCTGT	985
Qy	841	ATAATGCTGGGAGGATGCCAATTGAAAGATGATGGCTAAAGAAAGCCTTATTCTCAA	900
Db	986	ATAATGCTGGGAGGATGCCAATTGATGTTGATGGCTAAAGAAAGCCTTATTCTCAA	1045
Qy	901	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	960
Db	1046	CTGCCAATGGACTGTTTACAATGCCATCTTATTCCAGACGCATTCCACAGCTACACCA	1105
Qy	961	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGAGCACTCAGAATA	1020
Db	1106	TATATGAATGGAGAACATCTACAAAATCCCTTGGGTATAATAGTGCACTCAGAATA	1165
Qy	1021	AAAATTCTTGCAACCTACGTGAATCTAAATATTGAGACATTGACAAGATTATGTT	1080
Db	1166	AAAATTCTTGCAACCTACGTGAATGTAATATTGAGACATTGATAAGATCTATGTT	1225
Qy	1081	CGAACAGGTATCTACCAGGAGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1140
Db	1226	CGAACAGGTATCTACCAGGAGAGAACCTTATGTGACAATGTGAAACACTCAAAGAGTA	1285
Qy	1141	CCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1200
Db	1286	CCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATACATTCTGATCTT	1345
Qy	1201	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1260
Db	1346	CCTCGTGTGCTCGACTTGCCTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGTAAA	1405
Qy	1261	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1320
Db	1406	GAGGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGATTACACAGACACTCTA	1465
Qy	1321	GTATCTGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1380

Db	1466	GTATCTGGAAAAATGGCTTGAATCTTGCCAGTACCTCATGGATTAGAAGATTGCTG	1525
Qy	1381	AACCTATTGGTGTACTGGATCAAATCCAATAAGAACTCCATGCTTAGAGTTGGAG	1440
Db	1526	AACCTATTGGTGTACTGGATCAAATCCAATAAGAACTCCATGCTTAGAGTTGGAG	1585
Qy	1441	TTTGAUTGGTTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1500
Db	1586	TTTGAUTGGTTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTGATTGAAGAGCATGCC	1645
Qy	1501	AATTGGTCTGTATCCCGAGAACGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1560
Db	1646	AATTGGTCTGTATCCCGAGAACGCAGGATTAGCTATTCCCACGCAGGACTGAGTAACAGA	1705
Qy	1561	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGAACAGCTCAAAGCAATTCTACA	1620
Db	1706	CTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGAACAGCTCAAAGCAATTCTACA	1765
Qy	1621	CGAAATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1680
Db	1766	CGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTCTATGGAGTCACAGACAC	1825
Qy	1681	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGGAATTCT	1740
Db	1826	TATTGTGTAACTATCCCCGAAATTCTACCCAAATTGCTCTGTCTGTTAAATGGAATTCT	1885
Qy	1741	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCTCCAATCAAACCTGAA	1800
Db	1886	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCTCCAATCAAACCTGAA	1945
Qy	1801	CAGGCTATGAAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	1860
Db	1946	CAGGCTATGAAACTTCTGGACTGTAATTACCCAGATCCTATGGTCGAGGTTTGCTGTT	2005
Qy	1861	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTAGCTAGTA	1920
Db	2006	CGGTGCTTGGAAAAATTTAACAGATGACAAACTTCTCAGTATTAAATTAGCTAGTA	2065
Qy	1921	CAGGCTCTAAATATGAACAATATTGGATAACTGCTTGTGAGATTAACTGAGAAA	1980
Db	2066	CAGGCTCTAAATATGAACAATATTGGATAACTGCTTGTGAGATTAACTGAGAAA	2125
Qy	1981	GCATTGACTAATCAAAGGATTGGCAGTTTCTTGGCATTAAATCTGAGATGCAC	2040
Db	2126	GCATTGACTAATCAAAGGATTGGCAGTTTCTTGGCATTAAATCTGAGATGCAC	2185
Qy	2041	AATAAAACAGTTAGCCAGAGGTTGGCCTGCTTGGAGTCCTATTGTCGTGCATGTGGG	2100

Db	2186	AATAAAACAGTTAGCCAGAGGTTGGCTGCTTGGAGTCCTATTGCGTGATGTGGG	2245
Qy	2101	ATGTATTGAAAGCACCTGAATAGGCAAGTCAGGCAATGGAAAAGCTCATTAACCTA	2160
Db	2246	ATGTATTGAAAGCACCTGAATAGGCAAGTCAGGCAATGGAAAAGCTCATTAACCTA	2305
Qy	2161	GACATTCTCAAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2220
Db	2306	GACATTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTAGTT	2365
Qy	2221	GAGCAAATGAGGCGACCAGATTCTATGGATGCCCTACAGGGCTTGCTGTCCTCTAAAC	2280
Db	2366	GAGCAAATGAGGCGACCAGATTCTATGGATGCTACAGGGCTTCTGTCCTCTAAAC	2425
Qy	2281	CCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTCTGC	2340
Db	2426	CCTGCTCATCAACTAGGAAACCTCAGGCTTGAAGAGTGTGCAATTATGCTCTGC	2485
Qy	2341	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTT	2400
Db	2486	AGGCCACTGTGGTTGAATTGGGAGAACCCAGACATCATGTCAGAGTTACTGTT	2545
Qy	2401	AATGAGATCATTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2460
Db	2546	AATGAGATCATTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTCAAATT	2605
Qy	2461	ATTCGTATTATGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2520
Db	2606	ATTCGTATTATGAAAATATCTGGAAATCAAGGTCTGATCTCGAATGTTACCTTAT	2665
Qy	2521	GGTTGTCGTCAATCGTGACTGTGTTGGACTTATTGAGGTGGTGC	2580
Db	2666	GGTTGTCGTCAATCGTGACTGTGTTGGACTTATTGAGGTGGTGC	2725
Qy	2581	ATTATGCAAATTCACTGCAAAGGCGGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2640
Db	2726	ATTATGCAAATTCACTGCAAAGGCGGTTGAAAGGTGCACTGCAGTTAACAGCCACACA	2785
Qy	2641	CTACATCACTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2700
Db	2786	CTACATCACTGGCTCAAAGACAAGAACAAAGGAGAAATATGATGCAGCCATTGACCTG	2845
Qy	2701	TTTACACGTTCATGTGCTGGATACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2760
Db	2846	TTTACACGTTCATGTGCTGGATACTGTGAGCTACCTTCATTTGGAAATTGGAGATCGT	2905
Qy	2761	CACAATAGTAACATCATGGTAAAGACGATGGACAATGTTCATATAGATTGGACAC	2820
Db	2906	CACAATAGTAACATCATGGTAAAGACGATGGACAATGTTCATATAGATTGGACAC	2965

Qy	2821	TTTTGGATACAAGAAGAAAAATTGGTATAAACGAGAACGTGTGCCATTGTTTG	2880
Db	2966	TTTTGGATACAAGAAGAAAAATTGGTATAAACGAGAACGTGTGCCATTGTTTG	3025
Qy	2881	ACACAGGATTCTTAATAGTGATTAAAGGAGCCAAAGAACATGCACAAAGACAAGAGAA	2940
Db	3026	ACACAGGATTCTTAATAGTGATTAAAGGAGCCAAAGAACATGCACAAAGACAAGAGAA	3085
Qy	2941	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT	3000
Db	3086	TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTGACAGCATGCCAAT	3145
Qy	3001	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTT	3060
Db	3146	CTCTTCATAAAATCTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTT	3205
Qy	3061	GATGACATTGCATACATTGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3120
Db	3206	GATGACATTGCATACATTGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTG	3265
Qy	3121	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3180
Db	3266	GAGTATTCATGAAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAAATGGAT	3325
Qy	3181	TGGATCTCCACACAATTAAACAGCATGCATTGAACTG-AAAGATAACTGAGAAAATGAA	3239
Db	3326	TGGATCTCCACACAATTAAACAGCATGCATTGAACTGAAAAGATAACTGAGAAAATGAA	3385
Qy	3240	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3299
Db	3386	AGCTCACTCTGGATTCCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGC	3445
Qy	3300	ATAGGAATTGCACAATCCATGAACAGCATTAG-ATTTACAGCAAGAACAGAAATAAAATA	3358
Db	3446	ATAGGAATTGCACAATCCATGAACAGCATTAGAATTACAGCAAGAACAGAAATAAAATA	3505
Qy	3359	CTATATAATTAAATAATGAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATT	3418
Db	3506	CTATATAATTAAATAATGAAACGCAAACAGGGTTGATAGCACTTAAACTAGTTCAATT	3565
Qy	3419	TCAAAA 3424	
Db	3566	TCAAAA 3571	

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